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-Q=/Ggn2 1/USPTO spool/US09720086/runat 18112002 092957 29457/app_query.fasta_1.4252
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09720086 @CGN 1 108 @runat 18112002 092957 29457 -NCPU=6 -ICPU=3
-NO XLPXY -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPOFS -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 200000000
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-MODEL=frame+_p2n.model -DEV=xlh
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Ygapop 10.0 , Ygapext
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               Listing first 45 summaries
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Copyright (c) 1993 - 2002
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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4190
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           US-09-276-531-47
US-08-924-345-1
US-08-814-095-7
US-08-804-227C-1
US-09-295-593-37
US-08-458-568A-11
US-09-154-750A-75
US-08-061-376-4
US-08-327-392-1
US-08-326-6518-55
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Compugen Ltd
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Sequence 1, Appli
Sequence 37, Appl
Sequence 11, Appl
Sequence 4, Appli
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ALIGNMENTS

GENERAL INFORMATION: APPLICANT: Bandman

Bandman, Olga

APPLICANT:

APPLICANT:

Lal, Preeti Hillman, Jennifer

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APPLICANT:
APPLICANT:
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: March 2'
CLASSIFICATION:
                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,531
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING

TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
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                                                                                               FILING DATE: H
CLASSIFICATION:
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CITY: PALO ALTO
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                                     March 27, 1998
                                                                                                                   Herewith
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723 ThrGlyArgLeuPhePheGluPheTyrArgLeuLeuHisAspAlaArgProLysGluGly 742
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REGISCONGUISCACCHOCKER PA-0008 US
TELECOMMUNICATION INPORMATION:
TELEPHONE: (650) 855-0555
TELEPAK: (650) 845-4166
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2077 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TESTIUT02
CLONE: 1271435
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748.00
81.95%
73.66%
15.24%
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Query Match:
DB:
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US-08-924-345-1
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Sequence, h. Application US/0992435

SEGREAL INFORMATION: CASASTELOS ISABLIE, Christine, Marie-Andree - APPLICANT: LENG-TEACTS ISABLIE, Christine, Marie-Andree - APPLICANT: LENG-TEACTS ISABLIE, Christine, Marie-Andree - APPLICANT: ALINDONNE TARK MICHO. Emple, Francis and Vaccinse of the Infectious INTEREST: TARENTION: Bovins Phinocrachetis virus CHRESCOREST AND TAYLOR STREET: TAYLOR THE TAYLOR STREET: TAYLOR AND TAYLOR STREET: TAYLOR THE TAYLOR THE TAYLOR STREET: TAYLOR THE THORWATION: Standard name = "BHV.1 gF" TAYLOR THORWATION: THE TAYLOR THE THORWATION: Standard name = "BHV.1 gF" TAYLOR THORWATION: THE TAYLOR THORWA
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Qy 278 ProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeuValTrpGlyLysLeuArg 297 Db 1695CCCGGGCTCGGCTTCGGTCGACACGGTCTTCACGGCGCGCGC	Db 1659 CGGGCTGATGGCCGAGGCCGAGCCCGCAACC 1694	Qy 263GlyAspAlaGlyAspLysAsnAlaThrLysAlaAlaAspAspGlu 277	Qy 247 ThrAspProAlaSerProThrValAlaThrThrProGluProValGly 262		Qy 227 GlnAlaSerGlyGluSerGlnLysValGluGluAlaSerProProAlaValGlnGlnPro 246	Qy 208 ArgGluAlaGluLysLysAlaLysValIleAlaValMetAsnAlaValGluGluAsn 226	Db 1431 GCGTTGAGCGGCCGACCGCCGGCTGTTAAATGGGTCTCGCGCGCG	Oy 190 AspProTyrTyrIleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLys 207	Db 1371 CGGGGTGGGGAAAGCCGGAGGAAGACCGGGGGAGCTGCGTGGAGGGCGGA 1430			Qy 154 IleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGly 169	1254 CGTCGTGGCACTGGGCTCCCGGCCAAAGGCGCCCCCCCTCGCCACCATCAGCGAAGA	Qy 135 ThrLysGluGlyArqGlyAlaSerAlaGlyGluGlyLysGluGlnLysGlnThrAsn 153	1227 CGGCGCGACCGAGCCCCAGCCAC	115 GlvGlvGhrGlvThrGlvThrDroGlvAlaecarargalaValGlvAsnGlvCvsCvsVal	Db 1167 CAAGCCGCGGACGTGCGCGCGCGCGACGCACTTGCGCGCGC	יין בין ביים בין	Db 1116 GGTAAACTGCGCGCTGCGCGTCGCTGCTGCTGCCGTGCTCTCGGCGCGTTTA 1166	70	OY 64 LYSASPEROALAVALTHATHATLYSSEEGLEPROMERALAGIN77	996 CCCGGCCGCTGCGCAGCCGGCCGGAACACGCCCGCTCGCT	48 ProGlyArgLysArgLysHisProProValGluSerSerAspThrPro	939	Qy 35ArgGlnGluProSerAlaThrAlaArgLysValGlyArg 47	Db 879 GACGACGGAAGTCGAĞĞCCGCGACĞAĞAGCGGGCTCGGCGTTTGCCCCTCACCACGCCCCC 938	SCCCCAC	Qy 6 ProGlyAspThrSerSerSerSerLeuGluArgGluAspAspArgLysGluGlyGluGlu 25	US-09-720-086-5 (1-908) x US-08-924-345-1 (1-4190)	Best Local Similarity: 22.04% Mismatches: 212 Query Match: 3.36% Indels: 151 DB: Gaps: 24
REGISTRATI REFERENCE TELECOMMUNICATION	; CLASSIFIC; ; ATTORNEY/AG;	; APPLICATION ; FILING DAG	OPERATING SOFTWARE:	COMPUTER RES MEDIUM TY COMPUTER:	; COUNTRY:	; STREET: ; CITY: Fax ; STATE: M:	; NUMBER OF S ; CORRESPONDE ; ADDRESSEE	; TITLE OF IN	; APPLICANT:	; GENERAL INFOR	; Sequence 7, App. ; Patent No. 6029	RESULT 3 US-08-814-095-7/	Db 2190 CGGGCC	Qy 442 aAlaTy:	Db 2169 CGAGGAG	Qy 422 uGluGl	Db 2127 GCTGCA	Qy 402 tileGl	Db 2070 CCTGTA	ОУ 389	Db 2010 TCGCAAC	Qy 372 aSerSe	Db 1950 CGACTC	352	1890	3 3 4	 72F	Db 1770 GCGCCC	1743	298

US-08-814-05-7/c

; Sequence 7, Application US/08814095

Patent No. 6025183
; GENERAL INFORMATION:
APPLICANT: SOYEG, HEYMONA
APPLICANT: SOYEG, HEYMONA
APPLICANT: SCOYEG, HEYMONA
APPLICANT: SCOYEG, HEYMONA
APPLICANT: SCOYEG, HEYMONA
APPLICANT: SOYEG, ANTI-CHOLINESTERASE SUBSTNACES
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: KOHN & ASSOCIATES
STREET: 30500 NO. 6025183thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/814,095
FILING DATE:
APPLICATION NUMBER: US/08/814,095
FILING DATE:
CLASSIFICATION NUMBER: US/08/814,095
FILING DATE:
CLASSIFICATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TTELECOMMUNICATION INFORMATION:

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CONTION: Complement (14529.,3485)

CHERN INFORMATION: function= "executic resistance of the complement (1402.,3456)

OTHER INFORMATION: funche= 1

FRATURE: CAND (1402.,34356)

OTHER INFORMATION: funche= 2

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OTHER INFORMATION: funche= 3

CONTION: Complement (13179.,33363)

OTHER INFORMATION: funche= 3

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OTHER INFORMATION: funche= 5

FRATURE: INFORMATION: funche= 5

CONTION: Complement (13259.,3304)

OTHER INFORMATION: funche= 5

NAME/KRY: exon

LOCATION: complement (13259.,3304)

OTHER INFORMATION: funche= 6

FRATURE: INFORMATION: funche= 6

FRATURE: COMPLEMENT (13269.,3304)

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FRATURE: COMPLEMENT (13269.,3304)

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OTHER INFORMATION: funche= 17

FRATURE: COMPLEMENT (13369.,3304)

OTHER INFORMATION: funche= 13

FRATURE: COMPLEMENT (13369.,3304)
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                                                                                                                                       217 IleAlaValMetAsnAlaValGluGluAsnGlnAlaSerGlyGluSerGlnLysValGlu 236
269 nAlaThrLysAlaAlaAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIleGl 289
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                                                                                                                                                                                                                                                                            ArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLysLysAlaLysVal 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----LeuProAsnGlyAspLeuGluLysArgSerGluProGlnProGluGluGly 101
                                                                                                                                                                                                                                                                                                                                                                                                                Gly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GlyLysGluGlnLysGlnThrAsnIleGluSerMetLysMetGlu 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCACCCAGGAGCCAGAGGAGGAGGAGAAGGAGTGGGGAAGCCAGGGAAGGCGTGTGCAGC 24130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProGluAlaSerArg----- 133
                                                                           AlaSerProThrValAlaThrThr-ProGluProValGlyGlyAspAlaGlyAspLysAs 269
                                                                                                                                                                                                                                               AGAGGGAGGAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ValThrLysGluGlyArgGlyAlaSerAlaGlyGlu----- 145
                                                                                                                                                                                                                                                                                                                                                                                                           ---SerArgGlyArgLeuArgGlyGlyLeuGlyTrpGluSerSerLeu 176
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/number= 15
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                                                                                                                                                                                                                                                 -----GGAAGGAGACAGGCAGAGACAAGG------
                                                                                                                                                                                 ---ACACAGGCCAGCGGGCAGGAGGGGAAAGAGATC 23887
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Matches:
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623 23123	609HisaspGlnGluPheAspProProLysValTyrProProValPr	Db 2	
608 23183	594 gGluAspTrpProSerArgLeuGlnMetPhePheAlaAsnAsn	ОУ 2	
594 23243	574 uAspProTrpAsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeuArgArgAr 	Qу Db 2	
574 23267	557 uCysValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLysGl	р р 2	•
557 23308	537 sGlyGlyArgGluValLeuMetCysGlyAsnAsnAsnCysCysArgCysPheCysValGl	Oy Db 2	
23350	23350	Db 2	
537	517 eLeuGluCysAlaTyrGlnTyrAspAspAspGlyTyrGlnSerTyrCysThrIleCysCy	ş	
23350	23350	Db 2	
517	497 nValThrLeuGluHisProLeuPheIleGlyGlyMetCysGlnAsnCysLysAsnCysPh	Ş	
23350	23350	D b 2	
497	477 rGluValArgGlnLysCysArgAsnIleGluAspIleCysIleSerCysGlySerLeuAs	Ş	
23350	23373	2	
477	457 rThrGluLysBroLysValLysGluIleIleAspGluArgThrArgGluArgLeuValTy	ş	
23374		Db 2	
457	437 lGluProGluAlaAlaAlaTyrAlaProProProProAlaLysLysProArgLysSerTh	γQ	
23395	3425 TCGAGAGCCCCCCATCCGTCTGAAG	Db 2	
437	417 yLeuGluProProGluGluGluLysAsnProTyrLysGluValTyrThrAspMetTrpVa	Ş	
23426	3448	Db 2	
417	397 lGlnAsnLysGlnMetIleGluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGl	φ	
23449	3499 CGGGTTCCCATCAGO	N	•
397	LeupheProAlaCysHisAspSerAspGluSerAspSerGlyLysAlaValGluVa	Ş	
23500	3522CTGGCACCGAGCGCTGATGCCCG	Db 2:	
378		ş	
23523	3550	Db 2:	
358	338 uLysLeuMetProLeuSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGl	á	
23551	3610 TTCAGGGTGTGGAAGCCTCAGGTCCCCGGGGTCCCCCAAATCCTGCCTAGTCCACTCCCCA	Db 2:	
338	erValValCysValGl	Ş	
23611	3661 GCTCTCCTGGGTCGGCCAGACCCGGGGCCCTGGGGGGCGGTGGGCTGGGC	Db 2:	
326	ThrArgTrpValMetTr	γQ	
23662	3706 GCAGCGCCGCTGGGGGAGCTTGCGGCCTGAAGGCGCATCC	Db 2:	
306		Ş	
23707	13766 GGCACCAGAAGCCTCAGTCCACGAACAGGCCACCCGACAGGGGCGCGCGC	Db 23	

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---- 23083
623 oAla------GluLysArgLysProlleArgValLeuSerLeuPheAspGl 638
                                                                                                                                                 US-08-804-227C-1/c

Sequence 1, Application US/08804227C

Sequence 1, Application US/08804227C

Parent No. 576591

GENERAL INFORMATION:
APPLICANT: DeHoff Bradley S.
APPLICANT: RUBECOSS, Stuart A.
APPLICANT: Sutton, Kimberly L.
TITLE OF INFORTION: POLYKETIDE SYNTHASE GENES

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                      23122 CGCCGGTCACTCCTAGCCCAGCCCCGCCCCTGAGCGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                          Db 23082 ------GGGGTGGTGCTGCTGCTGGAGATT 23059
                                                                638 yIleAlaThrGlyLeuLeuValLeuLysAspLeu 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCI (DOS) TEXT Only
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/804,227C
FILING DATE: FEBRUARY 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy digk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUCENCE CITY 43280 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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OPERATING SYSTEM: MS-DOS
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14351..19945
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20010..31199
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36249..41774
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LOCATION: 816..14234
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LOCATION:
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LOCATION:
US-08-804-227C-1
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Pred. No.:
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23905 CCGTCCTCGAGGGGGGTCCGGCTCGTCGAGCGAGTCCAGACGGTC-GACCAGACC 23847
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                                                                                                                                                                                                                                        23786 CGGGACGGCGGGGGGCGCCACGAGCACGGCGGTCGGCGCTCGTTCGGCGAGCAGCGGTCCG 23727
                                                                                                                                                                                                                                                                                                                                     23726 CAGGGGGGGGGGGCGATCGGCCGGATCACGGCCACGGTCACCCGTGCCGCCACGCATCGGC 23667
                                                                                                                                                                                                                                                                                                                                                                                                                        23666 GAGTTCCTCCGGCAGCGGGCCGGAGAGTCCGGACAGGGTCACCCGCGTGCGCCGTTGCC 23607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23277 CGGCGCCGCGGGTCACCGCCCACCAGCCGGCCTCCGCGCGCCTGGCCTGGA 23218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23157 CGTGGTCCCCGGCCAACGCCAGCAGCGAGCGCTCCCGCGCAGCGGCCCGGCCTTCGTCCC 23098
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                                                                                                                                                                                                            21 LysGluGlyGluGluGluGluGluAsnArgGlyLys------GluGluArgGln 36
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                                     2 ProserSerGlyProGlyAspThrSerSerSerLeuGluArgGluAspAspArg--- 20
                                                                                                                                                                                                                                                                                                                                                                                     56 oValGluSerSerAspThrProLysAspProAlaValThrThrLysSerGlnProMet-- 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 -----AlaGlnAspSerGlyProSerAspLeuLeuProAsnGlyAspLeuGluLysAr 93
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US-09-720-086-5 (1-908) x US-08-804-227C-1 (1-43280)
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Best Local Similarity: Query Match:
DB:
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                                                                                                                     US-09-295-593-37
                                                          Score:
                                            Percent Similarity:
                                                                                                                                                                                 SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/295,593
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 60/082,791
EARLIER FILING DATE: 1998-04-23
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                              equence 37, Application US/09295593
atent No. 6417169
                                                                                                                                                                                                                                                                                                                                                                                                                                            09-295-593-37/c
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                                                                                                                              LENGTH: 4350
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR II ANTISENSE OLIGONUCLEOTIDE TITLE OF INVENTION: SEQUENCES AND METHODS OF USING SAME TO MODULATE CELL TITLE OF INVENTION: GROWTH FILE REFERENCE: 032396-046
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WRIGHT, Jim A. APPLICANT: YOUNG, Aiping H. APPLICANT: LEE, Yoon S.
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Mismatches:
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TCACTGCCCCCCTGTTACATGGGGGGGGGGGTTTAATTTGGTTTCTGAGCGCATAAAG---
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                                                                                                     GlnProThrAspProAlaSerProThrValAlaThrThrProGluPro------Val
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AspGlyArgGlyPheGlyIleGlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrp
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2675 GACGGGCAAAGATGATCCCTAGGTGTGCTCCGGTGGGGG------GGTCCCCAAGAT 2625
                                                               2624 CTTCCTTCCAGG-------AGCACAGGGAGTCAGGCTACTCGTGGG--- 2583
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                                                                                                 322 ArgTrpValMetTrpPheGlyAspGlyLysPhe------SerValValCysVal 337
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Patent No. 5821339
GENERAL INFORMATION:
APPLICANT: Schaffer, Priscilla A.
APPLICANT: Yeh, Lily
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Compositions and Methods for Treatment of Herpesvirus Infections
                                                                  ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
STREFT: One Liberty Place, 46th floor
CITY: Philadelphia
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| S994 GCGAGGCGCGCGGCGTCGGGATCGTCCGGACGGCCTCCTCCTACCATGG----- 6047
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/458,568A
FILING DATE: 02-JUNE-1995
CLASSIFICATION: 435
PHIOR APPLICATION: 435
PHIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,146
CLASSIFICATION OF 435
ATTORNEY/AGENT INFORMATION:
NAME: LEGRY DA.D., Kathryn R.
REGISTRATION NUMBER: 36,317
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
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Herpes Simplex Virus Type 1
                                                                                                                                                                     COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPACNE: (215) 568-3100
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 12001 base pairs
nucleic acid
EDNESS: double
TITLE OF INVENTION: COM
TITLE OF INVENTION: INF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                           USA
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US-08-458-568A-11
                                                                                                                                      COUNTRY:
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erAspSerGlyLys 393 GGTTCG 6965	374 SerArgAlaGlyLysLeuPheProAlaCysHisAspSerAspGluSe	29 gd
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euGlnValAlaSer 373	354 ThrTyrAsnLysGlnProMetTyrArgLysAlaIleTyrGluValLeuGlnValA	
laPheHisGlnAla 353 GTTCCGCATGCTA 6917	334 ValValCysValGluLysLeuMetProLeuSerSerPheCysSerAlaP	89 qd 70 g
6	855 CCGCCCCGCATGGCATCTCATTACCGC	Db 68
ърGlyLysPheSer 333	314 ArgSerArgAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAs	Qy 3
grederccececc 6854	822 -	Db 68
pTrpMetThrGly 313	294 GlyLysLeuArgGlyPheSerTrpTrpProGlyArgIleValSerTr	Qy 2
6821	807	Db 68
yGluLeuValTrp 293	274 AlaAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeuV	Qy 2
T 6806	759 GGGGGCCCGTGGCCGGGCCGGCCGAT	Db 67
nAlaThrLysAla 273	58ProGluProValGlyGlyAspAlaGl	2
r 257 	50 AlaSerProThrValAlaThrTh	Qy 2!
	648 GGGCCGGCGGAAGGAGGAGCAGCGGAGGCCGCCGGCC	Db 66
pPro 24 	30 GlyGluSerGlnLysValGluGluAlaSerProProAlaValG	Qy 2:
CCA 6647	21 GGGCGTCCTCGGGCTCATATAGTC	Db 662
uAsnGlnAlaSer 229	10	0у 21
ngı		δ. 10
LysArgGlu 209	00 Trp[enAlaArg	ن ن
GACGGTCTGTCTC 6560	16	Db 651
201	88 AlaGlyAspProTyr	Оу 18
CTTCGTC 6515	62	Db 646
gLeuThrPheGln 187	169 GlyLeuGlyTrpGluSerSerLeuArgGlnArgProMetProArgLeuThrPheGln	Оу 16
CGCGGACCGGTCG 6461	02	Db 640
vargheuargGly 168	149 GlnLysGlnThrAsnIleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGly	14
TGGGGGAGGG 6401		£
ıGlyLysGlu 148	133 CysValThrLysGluGlyArgGlyAlaSerAlaGlyGlu	0у 13
rccrccgggara 6341	282 AGCCGGGGCGCTGCTTGTTCTCCGACGCCATCGCCGATGCGGGGGCGATCCTCCGGGGATA	Db 628
lGluAsnGlyCys 132	113 AlaGluGlyGluGlyThrGluThrProProGluAlaSerArgAlaValGluAsnGlyCys	0у 11
TGGGGCCCGGGG 6281	2 CCCCCCCTCGTCGCGGTCTGGGCTCGGGGTG	Db 622
GlyGlyAlaPro 112	02	Qy 10
	2 GGTCGGGGTCGTGGTCGGGGTCGTCCCCGCCC	616
ProGluGluGly 101	95GluProGln	9

4 SerGI 	gnment Scores: d. No.: 15 re: 15 cent Similarity: 32 cent Similarity: 31 ry Match: 4 203-720-086-5 (1-908) x	RESULT 7 US-09-154-750A-75 US-09-154-750A-75 J Sequence 75, Application US/091547 Patent No. 6432640 GENERAL INFORMATION: APPLICANT: Vogelstein, Bert APPLICANT: Nogelstein, Bert APPLICANT: Polyak, Kornelia APPLICANT: Polyak, Kornelia APPLICANT: Polyak, Kornelia APPLICANT: 1107.75357 CURRENT APPLICATION NUMBER: 60/059, PRIOR APPLICATION NUMBER: 60/059, PRIOR APPLICATION NUMBER: 60/079, PRIOR FILING DATE: 1997-09-17 PRIOR APPLICATION NUMBER: 60/079, PRIOR FILING DATE: 1998-03-30 NUMBER OF SEQ ID NOS: 93 SOFTWARE: FASTSEQ for Windows Ver SEQ ID NO 75 LENGTH: 2608 TYPE: DNA ORGANISM: Homo sapiens US-09-154-750A-75	Oy 471 rArgGlu	451 7092	Qy 434 AspMetTrpValGluProGluAla- Db 7032 GACGCCGGGACCAACGGGACGGCGG	6966 414 6990	Qy 394 AlaValGluValGlnAsnLysG
AspThrSerSerSerLeuGluArGInGluGluAsnArgGl ACTGCAGTGAAGCGTGATGAACCAG ArgLysValGlyArgProGlyArgLy GGACGTGCAGGACCAGCTGACCAGCAGAACCAGGACCTCCAGCCCAGCCAAGAAA CCAGGAACTCCAGCCCAGC	0.0013 159.50 32.04* 21.13* 3.25* 4	lication US/09154750A (40 TON: TON: Istein, Bert Istein, Kenneth yak, Kornelia Yok, Kornelia TON: p53-Induced Apoptosis 1107.75357 INTON NUMBER: US/09/154,750A DATE: 1998-09-17 ION NUMBER: 60/059,153 ITE: 1998-09-17 ION NUMBER: 60/079817 ITE: 1998-03-30 ID NOS: 93 SEQ for Windows Version 3.0	rargGluargLeuValTyrGluValArgGlnLysCysArgAsn 485		AspMetTrpValGluProGluAla-AlaAlaTyrAlaProProProProAlaLy 451 	 GCGGTAATGAGATACGAGCCCCGC 6989 GlyProLysGlyLeuGluProProGluGluGluLysAsnProTyrLysGluValTyrThr 433 GCGCCCGTTGGCCGTCCCCGGGCCCCCCGGTCCCGGCCGG7031	AlaValGluValGlnAsnLysGlnMetIleGluTrpAlaLeuGlyGlyPheGlnProSer 413

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971 GGAGAGCGCACTGCGGGAGATGAGAGAGCCAACGGGCTGCTCCAGGA------- 1018
                                                                                                                                                                            1019 ---AGAGCTGGAAGGCTGCAGAAGCTGGGGCGCCAGGAGAAGATGCAGGAGACGCT 1075
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1076 GGTTGGCTTGGAGCTGGAGAGAGGCTGCTGGCCAAGCTGCAAAGCTGGGAAGACT 1135
                                  911 CATGAAGTCTGAGCTGGTACGCCTCCCTAGGCTGGAACGGGAGCTGGAGCAGCTGGAGCA 970
                                                                       GlyGluGlyThrGluThrProProGluAlaSerArgAlaValGluAsnGlyCysCysVal 134
                                                                                                                                          135 ThrLysGluGlyArgGlyAlaSerAlaGlyGluGly-LysGluGlnLysGlnThrAsnIl 154
                                                                                                                                                                                                                                                                                                                                                                                            1183 -------GATTCGTGGTTGAGCTG-CAGC 1203
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1204 AGAGGGAGCTTGCCTTGAAGGACAAGAACAGCGCCGTCAC------CAGCAGCGCC 1253
96 ProGlnProGluGluGly---SerProAlaAlaGlyGlnLysGlyGlyAlaProAlaGlu 114
                                                                                                                                                                                                                 154 eGluSerMetLysMetGluGlySerArg-----GlyArgLeu-ArgGlyGlyGlyT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1254 CGGGGGCTGGAGAAGCCCAGCCAGCAGCAGCAGGAGGAGCTCCGGCAGGTCAGGCGGCCAG 1313
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APPLICANT: Evans, Glen A. Malek APPLICANT: Djabali, Malek APPLICANT: Djabali, Malek APPLICANT: Djabali, Malek APPLICANT: Selleri, Licia APPLICANT: Parry, Pauline TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11023
TITLE OF INVENTION: TRANSLOCATION BREAKPOINT ASSOCIATED WITH ACUTE LEUKEMIAS NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                     1832 GGCCAGGCACCTGCGCGAAGACCACACACCA------GCTGCAGGCGGAGTGCGA 1882
                                                                                                                  1883 GCGACTGCGGGGCTCCTGCGCGCCATGGAGAGGAGGCACCGTCCCCGCCGA----- 1936
                                                                                                                                                                                    1937 ------CTTTGAGGCTGCCGCGCGAGTCGCCATCGTCCAAGGA 1975
                                                                                                                                                                                                                                                                     1976 GGTGGCAGAGCTGAAAGCAGGTGGAGAGTGCCGAGCTGAAGAACCAGCGGCTCAAGGA 2035
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392 GlyLysAlaValGluValGlnAsnLysGlnMetIleGluTrpAlaLeuGlyGlyPheGln 411
                                                                            412 ProSerGlyProLysGlyLeuGluProProGluGluLysAsnProTyrLysGluVal 431
                                                                                                                                                       432 TyrThrAspMetTrpValGluPro-GluAlaAlaAlaArAlaProProProPro---- 449
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                                                                                                                                                                                                                                                                                                           465 ullelleAspGluArgThrArgGluArgLeuValTyrGļuValArgGlnLysCysArgAs 485
                                                                                                                                                                                                                                                                                                                                                                                       485 nlleGluAsplleCysileSerCysGlySerLeuAsn---------ValTh 499
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STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
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Patent No. 6175000
GENERAL INFORMATION:
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DB;
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-720-086-5 (1-908) x US-08-061-376-4 (1-11907)
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/061,376

FILLING DATE: 13-MAY-1993

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9387

TELEPHONE: (619)546-4737

TELEPHONE: (619)546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (619)546-9392

WFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11907 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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                                                                       2940 ATCCCTGGAGAAGGAAAACCCCTCTGCCTTTCCACTCCTTCATCTAGCACTGTTAAACA 2999
                                                                                                                                                                                                                     2880 TATAAAGAAAGGGAGAGGAAATCTGGAAAAAAACCAACTTGGACCTCGGCCCAACTGCCCC
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                                                                                                                                                                               113 AlaGluGlyGluGlyThrGluThrProPro----
                                  130 AsnGlyCysCysValThrLysGluGlyArgGlyAla-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 ThrAlaArgLysValGlyArgProGlyArgLysArg---LysHisProProValGluSer 59
                                                                                                                                                                                                                                                                                                                                                                                             60 SerAspThrProLysAspProAlaValThrThrLysSerGlnProMetAlaGlnAspSer 79
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TOPOLOGY: unl
                                                                                                                                                                                                                                                         93 ArgSerGluProGlnProGluGluGlySerProAlaAlaGlyGlnLysGlyGlyAlaPro 112
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                                                                                                                                                                                                                                                                                            GGGACTGATATTACTTCTGTGACTCTTGGGGGATACAACAGCTGT-CAAAACCAAAATACT 2879
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32.17%
19.12%
3.23%
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                                                                                                       -----GluAlaSerArgAlaValGlu 129
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148
101
275
254
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451 STANDERORY CORRESPONDED TO THE PROPERTY OF	?
AAAGCAGCCTCCAC	рb
431 TyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProProProProAlaLy 451	Qy
CCAGCCAGCACTGGTCATCCCGCCTCAGCCACCTACTACAGGACCGCCAAGAAAAGAAGT 39	ъ В
420ProFroGluGluLysAsnProTyrLysGluVa 431	Š
413 FGTYFTOLYSGTYFEUGIU	B 5
413 rGlybrofyroGlyr angly	? !
393 sAlaValGluValGlnAsnLysGlnMetIleGluTrpAlaLeuGlyGlyPheGlnProSe 413	음 성
33 CCATCAGCAAGAGAGGATCCTGCCCCAAAG-AAAAGCAGTXGTGAGCCTCCTCCACGAAA 37	문
77GlyLysLeuPheProAlaCysHisAspSerAspGluSerAspSerGlyLy 39	8
3673 AAAGACAGCAAAGAGAGCAGTGTTGTGAAGAACGTGGTGGACTCTAGTCAGAAACCTACC 3732	рb
370 nValAlaSerSerArgAla 376	δ
TAAAGCTGTGAAAA-AGAAAGAGAAA	뮍
laThrTyrAsnLysGlnProMet	Ş
CAGTGCTGCAAGATGAGAAAATGTCAGAATCTACAAT	망
332 eSerValValCysValGluLysLeuMetProLeuSerSerPheCysSerAlaPh 350	Ş
3509 CTAATTGCTTAGATAAGCCCAAGTTTGGTGGTCGCAATATAAAGA 3553	맔
laGluGlyThrArgTrpVal	ઇ
CTGCCAGGTGCCTGAGGACTGTG	뫄
lyPheSerTrp	δδ
3411 CAAGGCACCCCAGGAACCTCCAGTAAAGAAAGGACGTCG-ATCGAGGCGGT 3460	Db
yPheGlyIl	Ş
3399 TGTCACTAGAAA 3410	윱
252 oThrValAlaThrThrProGluProValGlyGlyAspAlaGlyAspLysAsnAlaThrLy 272	Ś
3355GAAGATGCTGAACCTCTTGCTCCACCCATCAAACCAATTAAACC 3398	Дb
232 rGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAspProAlaSerPr 252	ş
3297 ACGAGAAAAGATTTTGTCTTCCATGGGGAATGATGACAAGTCATCAATTGCTGGCTCA 3354	DЬ
LysAlaLysValIleAlaValMetAsnAlaValGluGluAsnGlnAlaSer	ş
3280GCCTTACCATGGGAAGA 3296	DЪ
	Ş
3240 AAAACGAGCIGIGTTTCCTGATGACATGCCCACCCTGAGT 3279	망
172 pGluSerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTy 192	δ
3180 CTCTGTGCGAGGACCCCGGATTAAACATGTCTGCAGAAGAGCAGCTGTTGCCCTTGGCCG 3239	₽
.snIleGluSerMetLysMet	Ş
3120 GAGTCTTAAACAAACCGACCAGCCCAAAGCACGGGTCAAGAAAGTGACTCATCAGAGAC 3179	DЪ
142SerAlaGlyGluGlyLys-GluGlnLysGlnTh 152	Ś

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4128 GAACATCCTCGGCACTCTCTCCCAATGGCAATAGTTCTAAGCAAAAAATTCCAGCAGATGG 4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4068 AAAACCAAAAGAAAAGGAAAAACCACCTCCGGTCAATAAGCAGGAGAATGCAGGCACTTT 4127
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                                                                                                                                                                                                                                                                                                                                                                                                                                              4248 GGGAGGCTTAGGAATCTTGACTTCTGTTCCTATAACACCCCAGGGTGGTTTGCTTTCTCTG 4307
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                                                                                                                                                                                                                                                                                      473 ----GluArgLeuValTyrGluValArgGlnLysCys-----ArgAsnIleGluAsp-- 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              493 sGlySerLeuAsnValThrLeuGluHisProLeuPheIleGlyGlyMetCysGlnAsnCy 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       513 s------LysAsnCysPheLeuGluCysAlaTyrGlnTyrAspAspGl 528
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Patent No. 5633135

GENERAL INFORMATION:
APPLICANT: Crore, Carlo
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the TITLE OF INVENTION: All-1 Region
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSES: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
CITT: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               528 yTyrGlnSerTyrCysThrIleCys------CysGly-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     539 -GlyArgGluValLeuMetCysGlyAsnAsnAsnAsnCysCysArgCysPheCysValGluCy
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: 1BM FS/2
OPERATING SYSTEM: PC-DOS
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                                                                          459 uLysproLysValLysGlu-------
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SOFTWARE: WORDPERFECT 5.1
SOFTWARE: WORDPERFECT 5.1
APPLICATION NUMBER: US/08/320,559
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2638 GGGACTGATATTACTTCTGTGACTCTTGGGGATACAACAGCTGT-CAAAACCAAAATACT 2696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2584 TCATCTTCTGCCAAA----AAAGCAACAGGGCGGAAGAAGTCTTCATCATGATTCT 2637
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Matches:
Conservative:
Mismatches:
Indels:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993
FILING DATE: 14 MAY 1993
PRIOR APPLICATION NUMBER: US/07/971,094
FILING DATE: 30-0CT-92
PRIOR APPLICATION NUMBER: US/07/888,830
FILING DATE: 27-MAY-92
PRIOR APPLICATION NUMBER: US/07/888,830
FILING DATE: 11-DEC-91
APPLICATION NUMBER: US/07/805,093
FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
NAME: DGIANG MAYENTER
                                                                                                                                                                                                                                                                          ATTORNET DELUCA, MARK
NAMB: DeLUCA, MARK
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: TJU-C
TELECOMMUNICATION INPORMATION:
TELEFAX: (215) 568-3439
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14255
TYPANDENESS: single
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158.50
32.17#
19.12#
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; ANTI-SENSE: NO
US-08-320-559-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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RESULT US-OQU Seque Pates PATT TT	0y 4 0y 0b 4	- 4.	Др. 4 Ду Др. 4	Оу Оу Оу	Оу Оу Оу Ор Ф 4	Qy 3:	Db 37 OY 4 Db 38 OY 4 Db 38
SSULT 10 :-08-327-392-1 Sequence 1, Application US/08327392 Patent No. 5633136 GENERAL INFORMATION: APPLICANT: Croce, Carlo ALL-1 Polynucleotides and Monoclonal TITLE OF INVENTION: ALL-1 Polynucleotides and Monoclonal TITLE OF INVENTION: Treatment TUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS: ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5633136ris STREET: One Liberty Place - 46th Floor CITY: Philadelphia STATE: PA COUNTRY: USA ZIP: 19103 COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE COMPUTER: IBM OPERATING SYSTEM: PC-DOS SOFTWARE: WORDPERFECT 5.1	389 GATCTGTACCAAGTGTGTTCGCTGTAAGAGCTGTGGATCCACAACTCCAGGCAAAGGGTG 4448 597 pProSerArgLeuGlnMetPhePheAlaAsnAsnHisAsp 610	58 sValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTr 577	27 GGAAAATTGGTGTTGTCGTCGTTGCAATTCTGTCACGTTTTGTGAAGGCAACATCAGGC 4 39 -GlyArgGluValLeuMetCysGlyAsnAsnAsnCysCysArgCysPheCysValGluCy 5 31 -:::::::	513 sLysAsnCysPheLeuGluCysAlaTyrGlnTyrAspAspAspG1 528	489	466IleIleAspGluArgThrArg	71 TCCCAAAACCACTCCTAGTGAGCCCAAGAAAAGCAGCCTCCACCACCAGAATC 38 51 SLYSProArgLysSerThrThrG1 45 51 SLYSProArgLysSerThrThrG1 45 25 AGGTCCAGAGCAAACAGAAAAAAAGTGGCTCCCCGGCCCAAGTATCCCTGTAAAACA 38 59 ULYSProLysValLysGlu

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2524 GCTTTGTATCCTGTGGGTAGGGTTTCCAAAGAGGTTGTTGGTGAAGATGTTGCCACT 2583
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-720-086-5 (1-908) x US-08-327-392-1 (1-14255)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,392
FILING DATE:
PILING DATE:
APPLICATION: 435
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 07/971,094
FILING DATE: 30-0CT-92
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/88,830
FILING DATE: 11-DEC-91
APPLICATION NUMBER: 07/805,093
FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-310
TYPE: nucleic acid
STAPE: nucleic acid
STAPE: nucleic acid
STAPE: No
ANTI-SENSE: No
US-08-327-392-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.0195
158.50
32.17%
19.12%
3.23%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity: 3
Best Local Similarity: 13
Query Match:
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QQ	2877 GAGGGTTGCCAGCCTCCTAAAAAAGGCCCAAAGCTCAGCTCTGCAAGATTGAGAAGAGTAA 2936
ò	142SerAlaGlyGluGlyLyg-GluGlnLysGlnTh 152
qq	2937 GAGICTIAAACAAACCGACCAGCCCAAAGGACAGGGICAAGAAAGTGACTCATCAGAGGAC 2996
ò	152 rAsnileGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTr 172
QΩ	30
ò	172 pGluSerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTy 192
qа	3057 AAAACGAGCTGTGTTTCCTGATGACATGCCCACCCTGAGT3096
ò	192 rTyrIleSerLygArgLygArgAspGluTrpLeuAlaArgTrpLygArgGluAlaGluLy 212
qq	3097GCCTTACCATGGGAAGA 3113
δ	212 siysAlaiysValileAlaValMetAsnAlaValGluGluAsnGlnAlaSerGlyGluSe 232
qq	3114 ACGAGAAAAGATTTGTCTTCCATGGGGAATGATGACAAGTCATCAATTGCTGGCTCA 3171
ò	232 rGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAspProAlaSerPr 252
д	3172GAAGATGCTGAACCTCTTGCTCCACCCATCAAACCAATTAAACC 3215
ò	252 oThrValAlaThrThrProGluProValGlyGlyAspAlaGlyAspLysAsnAlaThrLy 272
qq	3216 TGTCACTAGAAA 3227
ò	272 sAlaAspAspGluProGluTyrGluAspGlyArgGlyPheGlylleGlyGluLeuVa 292
QQ	3228 CAAGGCACCCCCAGGAACCTCCAGTAAAGAAAGGACGTCG-ATCGAGGCGGT 3277
δ	292 lrpGlyLysLeuArgGlyPheSerTrpTrpProGlyArglleValSerTrpTrpMetTh 312
q	3278 GTGGGCAGTGTCCCGGCTGCCAGGTGCCTGAGGACTGTGGTGTTTGTA 3325
ò	312 rGlyArgSerArgAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLysPh 332
Q	3326 CTAATTGCTTAGATAAGCCCAAGTTTGGTGGTCGCAATATAAAGA 3370
ò	332 eSerValValCysValGluLysLeuMetProLeuSerSerPheCysSerAlaPh 350
ΩP	3371 AGCAGTGCTGCAAGATGAGAAAATGTCAGAATCTACAATGGATGCCTTCCAAAGCCTACC 3430
ò	350 eHisGlnAlaThrTyrAsnLysGlnProMetTyrArglysAlaIleTyrGluValLeuGl 370
qq	3431 TGCAGAAGCTAAAGCTGTGAAAA-AGAAAGAAAAAGTCTAAGACCAGTGAAAAG 3489
ò	370 nValAlaSerSerArgAla 376
С	3490 AAAGAAAGGAAAGAGGAGCAGTTGTGAAGAACGTGGTGGACTCTAGTCAGAAACCTACC 3549
ò	377GlyLysLeuPheProAlaCysHisAspSerAspGluSerAspSerGlyLy 393
q	3550 CCATCAGCAAGAGGATCCTGCCCCAAAG-AAAGCAGTAGTGAGCCTCCTCCACGAAA 3608
ò	393 sAlaValGluValGlnAsnLysGlnMetIleGluTrpAlaLeuGlyGlyPheGlnProSe 413
qq	3609 GCCCGTCGAGGAAAGAGTGAAGAAGGGAATGTCTCGGCCCC 3650
ò	413 rGlyProLysGlyLeuGlu
셤	3651 TGGGCCTGAATCCAAACAGGCCACCACTCCAGGAAGTCAAGCAAG
ò	420proTyrLysGluGluGluLysAsnproTyrLysGluVa 431
qq	3711 CCAGCCAGCACTGGTCATCCCGCCTCAGCCACCTACTACAGGACCGCCAAGAAAGA
ò	431 lTyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProProProProAlaLy 451
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US-08-306-691B-55
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                                                                                                                                                                                                                                                                                                                                           Sequence 55, Application US/08306691B Patent No. 5734039
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                      APPLICANT: Calabretta
APPLICANT: Skorski, T
TITLE OF INVENTION: A
TITLE OF INVENTION: C
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              SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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APPLICATION NUMBER:
                                                OPERATING SYSTEM: MS-DOS
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T: Two Penn Center,
Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: September CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2464
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rAsnIleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTr 172
                                            GAGTCTTAAACAAACCGACCAGCCCCAAAGCACAGGGTCAAGAAAGTGACTCATCAGAGAC
                                                                                                          GAGGGTTGCCAGCCTCCTAAAAAAGGCCCAAAGCTCAGCTCTGCAAGATTGAGAAGAGTAA
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                                                                                                                                        AsnGlyCysCysValThrLysGluGlyArgGlyAla------
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    SerAspLeuLeuProAsnGlyAspLeuGluLys

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엄	2997 CTCTGTGCGAGGACCCCGGATTAAACATGTCTGCAGAAGAGCAGCTGTTGCCCTTGGCCG 3056
ò	172 pGluSerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTy 192
g	3057 AAAACGAGCTGTTTCCTGATGACATGCCCACCCTGAGT3096
ò	192 rTyrIleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLy 212
qq	
දු ද	212 sLysalaLysValIleAlaValMetAsnAlaValGluGluAsnGlnAlaSerGlyGluSe 232
ò	rGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAspProAlaSerPr
QQ	3172GARGATGCTGAACCTCTTGCTCCACCCATCAAACCAATTAAACC 3215
ઠે	252 oThrValAlaThrThrProGluProValGlyGlyAspAlaGlyAspLysAsnAlaThrLy 272
q	3216 TGTCACTAGAAA 3227
ò	272 sAlaAbaAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeuVa 292
q	3228 CAAGGCACCCCAGGAACCTCCAGTAAGAAAGACGTCG-ATCGAGGCGGT 3277
ò	292 lTrpGlyLysLeuArgGlyPheSerTrpTrpFroGlyArglleValSerTrpTrpMetTh 312
qq	3278 GTGGGCAGTGTCCCCGGCTGCCAGGTGCCTGAGGACTGTGGTGTTGTA 3325
ò	312 rGlyArgSerArgAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLysPh 332
g	3326 CTAATTGCTTAGATAAGCCCAA
ò	332 eSerValValCysValGluLysLeuMetProLeuSerSerPheCysSerAlaPh 350
qq	3371 AGCAGTGCTGCAAGATGAGAAAATGTCAGAATCTACAATGGATGCCTTCCAAAGCCTACC 3430
ò	350 eHisGlnAlaThrTyrAbnLysGlnProMetTyrArgLysAlaIleTyrGluValLeuGl 370
g	3431 TGCAGAAGCAAGCTGTGAAAA-AGAAAGAGAAAAAGTCTAAGACCAGTGAAAAG 3489
ò	370 nValAlaSerSerArgAla 376
qq	3490 AAAGACAGCAAAGAGAGCAGTGTTGTGAAGAACGTGGTGGACTCTAGTCAGAAACCTACC 3549
ò	377GlyLysLeuPheProAlaCysHisAspSerAspGluSerAspSerGlyLy 393
qq	3550 CCATCAGCAAGAAGGATCCTGCCCCAAAG-AAAAGCAGTAGTGAGCCTCCTCCACGAAA 3608
ò	393 gAlaValGluValGlnAsnLysGlnMetIleGluTrpAlaLeuGlyGlyPheGlnProSe 413
qq	3609 GCCCGTCGAGGAAAGAGTGAAGAAGGGAATGTCTCGGCCCC 3650
ò	413 xGlyProLysGlyLeuGlu
QQ	3651 TGGGCTGAATCCAAACAGGCCACCACTCCAGCTTCCAGGAAGTCAAGCAAG
ò	420ProProGluGluGluLysAsnProTyrLysGluVa 431
qq	3711 CCAGCCAGCACTGGTCATCCCGCCTCAGCCACCTACTACAGGACCGCCAAGAAAGA
ò	431 lTyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProProProProAlaLy 451
qq	3771 TCCCAAAACCACTCCTAGTGAGCCCAAGAAAAAGCAGCCTCCACCACCAGAATC 3824
ò	451 8Ly8ProArgLysSerThrThrG1 459
qq	3825 AGGTCCAGAGCAGGAGCAAACAGAAAAAGTGGCTCCCCGCCCAAGTATCCCTGTAAAACA 3884
ò	459 uLysProLysVallysGlu465
QQ	3885 AAAACCAAAAGAAAAGGAAAAACCACCTCCGGTCAATAAGCAGGAGAATGCAGGCACTTT 3944

466	3945 GAACATCCTCAGCACTCTCCCAATGGCAATAGTTCTAAGCAAAAATTCCAGCAGATGG 4004	473GluargLeuValTyrGluValArgGlnLysCysArgAsnIleGluAsp 488		r b	luHisProLeuPhelleGlyGlyMetCysGlnAsnCy 513	1GCCAGIAGIGGGTATTGCCAAGICTG	513 s	528 yTyrGlnSerTyrCygThrIleCyg	4227 GGAAAATTGGTGTTGTCGTTGCAAATTCTGTCACGTTTGTGGAAGGCAACATCAGGC 4286	539 -GlyArgGluValLeuMetCysGlyAsnAsnAsnCysCysArgCysPheCysValGluCy 558	4287 TACAAAGCAGCTGCTGGAGTGTAATAAGTGCCGAAACAGCTATCACCCTGAGTG 4340	558 gValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTr 577	1341 CCTGGGACCAAACTACCCCACAAACCAAAGAAGAAGAAGAAGTCTG 4388	577 pAsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgGluAspTr 597	1389 GATCTGTACCAAGTGTTTGGCTGTAAGAGCTGTGGATCCACAACTCCAGGCAAAGGGTG 4448	rArgLeuGlnMetPhePhe	4449 GGATGCACAGTCTCATGATTTCTCACGTGTGTGAT 4488	12 545-860D-1		VFOR	Canami, Fili Formation Pilinetics measures	OF INVENTION: for Detection and Treatment of Acute Leukemias	Bulting rrom	Woodcock,	No. 6040140ris	1001	STATE: Pennsylvania COUNTRY: USA	9.6	MEDIUM TYPE: Floppy disk	63	SOFTWARE: Patentin Release #1.0, Version #1.25	APPLICATION NUMBER: US/08/545, 860D	SSIFICATION	PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/US94/04496	
	qΩ	<u>ک</u> و	i &	q Q	ò á		· 8 8	ò	옵	ò	op qu	ò	q q	ò	д	ογ	op qu	RESULT US-08-	; Sequ ; Pate	THI .							٠. ٠.			۰. ۰.					

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14255
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/971,094

FILING DATE: 30-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/888,839

FILING DATE: 27-MAY-1992

PRIOR APPLICATION UMBER: US 07/805,093

FILING DATE: 11-DEC-1991

APPLICATION NUMBER: US 07/805,093

FILING DATE: 11-DEC-1991

APPLICATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-1262

TELECHONE: (215) 568-3100

TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-720-086-5 (1-908) x US-08-545-860D-1 (1-14255)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/320,559
FILING DATE: 11-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,443
FILING DATE: 14-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: 334
APPLICATION NUMBER: US 08/327,392
FILING DATE: 19-OCT-1994
                                                                                                                                                                                                                                                                                                      2524 GCTTTGTATCCTGTGGGTÄGGGTTTCCAAAGAGAAGGTTGTTGGTGAAGATGTTGCCACT 2583
                                                                                                                                                                                                                                                                                                                                                                                2464 AATAAGCGGGAGTCAAGGAAAAGAGAAAAAGGGAATCAGAAATTCAGAGTAGTTCT 2523
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2757 ATCCCTGGAGAAGGAGAAACCCTCTGCCTTTCCACTCCTTCATCTAGCACTGTTAAACA 2816
                                                                                                                                                                                                                              2584 TCATCTTCTGCCAAA-----AAAGCAACAGGGCGGAAGAAGTCTTCATCACATGATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.:
                                    113 AlaGluGlyGluGlyThrGluThrProPro-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 SerSerSerLeuGluArgGluAspAspArgLysGluGlyGluGluGluGluGluAsn
                                                                                                                                                                                                                                                                                                                                     41 ThrAlaArgLysValGlyArgProGlyArgLysArg---LysHisProProValGluSer 59
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FILING DATE: 09-DEC-1992
                                                                       TATAAAGAAAGGGAGAGGAAATCTGGAAAAAAACCAACTTGGACCTCGGCCCAACTGCCCC 2756
                                                                                                              ArgSerGluProGlnProGluGluGlySerProAlaAlaGlyGlnLysGlyGlyAlaPro 112
                                                                                                                                                   GGGACTGATATTACTTCTGTGACTCTTGGGGÄTACAACAGCTGT-CAAAACCAAAATACT 2696
                                                                                                                                                                                           GlyPro-----
                                                                                                                                                                                                                                                                 SerAspThrProLysAspProAlaValThrThrLysSerGlnProMetAlaGlnAspSer 79
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32.17%
19.12%
3.23%
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                                                                                                                                                                                      -----SerAspLeuLeuProAsnGlyAspLeuGluLys 92
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Matches:
Conservative:
Mismatches:
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275
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3710	TGGGCCTGAATCCAAACAGGCCACCACTCCAGCTTCCAGGAAGTCAAGCAAG	3651	DЬ	
419	rGlyProLysGlyLeuGlu	413	Ş	
3650	GCCCGTCGAGGAAAAGAGTGAAGAA	3609	рb	
413		393	Qy	
3608	AAGCAGTAGTGAGCCTCCTCCAC	3550	Db	
393	GlyLysLeuPheProAlaCysHisAspSerAspGluSerAspSerGlyLy	377	ð	
3549	AAAGACAGCAAAGAGAGCAGTGTTGTGAAGAACGTGGTGGACTCTAGTCAGAAACCTACC	3490	망	
376	nValAlaSerSerArgAla	370	Qy	
3489	TGCAGAAGCTAAAGCTGTGAAAA-AGAAAGAGAAAAAGTCTAAGACCAGTGAAAAG	3431	망	
370	eHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLysAlaIleTyrGluValLeuGl	350	ν,	
3430	AGCAGTGCTGCAAGATGAGAAAATGTCAGAATCTACAATGGATGCCTTCCAAAGCCTACC	3371	рb	
350	eSerValValCysValGluLysLeuMetProLeuSerSerPheCysSerAlaPh	332	γQ	
3370	CTAATTGCTTAGATAAGCCCAAGTTTGGTGGTCGCAATATAAAGA	3326	Dъ	
332	ດ	312	γQ	
3325	Ω	3278	망	
312	lTrpGlyLysLeuArgGlyPheSerTrpTrpProGlyArgIleValSerTrpTrpMetTh	292	Qy	
3277	 GGAACCTCCAGTAAAGAAAGGAC	3228	В	
292	gGlyPheGlyIl	272	Qy	
3227	TGTCACTAGAAA	3216	몽	
272	oThrValAlaThrThrProGluProValGlyGlyAspAlaGlyAspLysAsnAlaThrLy	252	γQ	
3215	TIGCTCCACCCATCAAA	3172	망	
252	roProAlaValGlnGlnP	232	Qγ	
3171	GATTT	3114	DЬ	
232	LysAlaLysValIleAlaValMetAsnAlaValGluGluA	212	\$	
3113		3097	븅	_
212	C)	192	Qγ	
3096	AAAACGAGCTGTGTTTCCTGATGACATGCCCACCCTGAGT	3057	40	
192	pGluSerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTy	172	γ	
3056	CTCTGTGCGAGGACCCCGGATTAAACATGTCTGCAGAAGAGCAGCTGTTGCCCTTGGCCG	2997	라	
172	rAsnIleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTr	152	δ	
2996	GAGTCTTAAACAAACCGACCAGCCCAAAGCACAGGGTCAAGAAAGTGACTCATCAGAGAC	2937.	qq	
152	SerAlaGlyGluGlyLys-GluGlnLysGlnTh	142	Qy	
2936	GAGGGTTGCCAGCCTCCTAAAAAAGGCCAAAGCTCAGCTCTGCAAGATTGAGAAGAGTAA	2877	Db	
141	AsnGlyCysCysValThrLysGluGlyArgGlyAla	130	ργ	
2876	TTCCACTTCCTCCATAGGCTCCATGTTGGCTCAGGCAGACAAGCTTCCAATGACTGAC	2817	₽ B	
129	GluAlaSerArgAlaValGlu	123	δ 5	

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SECUREAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Cramani, Eli
TITLE OF INVENTION: Biagnostics, Therapeutics and Methods
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                          3825 AGGTCCAGAGCAGAGCAAACAGAAAAAGTGGCTCCCGCCCAAGTATCCCTGTAAAACA 3884
                                                                                                                                                                                                                                                                                                                   3885 AAAACCAAAAGAAAAGAAAAACCACCTCCGGTCAATAAGCAGAGAATGCAGGCACTTT 3944
                                                                                                                                                                                                                                                                                                                                                                                                  1945 GAACATCCTCAGCACTCTCTCAATGGCAATAGTTCTAAGCAAAAATTCCAGCAGATGG 4004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4167 TTGTGAGCCCTTCCACAAGTTTTGTTTAGAGAGAACGAGCGCCCTCTGGAGGACCAGCT 4226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4005 AGTCCACAGGATCAGAGTGGACTTTAAGGAGGATTGTGAAGCAGAAAATGTGTGGGAGAT 4064
                                                                                                                                                                               451 BLyBProArgLyBSer-----ThrThrGl 459
                                                                                                                                                                                                                                                                         473 ----GluArgLeuValTyrGluValArgGlnLysCys-----ArgAsnIleGluAsp-- 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           493 sGlySerLeuAsnValThrLeuGluHisProLeuPhelleGlyGlyMetCysGlnAsnCy 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      539 -GlyArgGluValLeuMetCysGlyAsnAsnAsnAsnCysCysArgCysPheCysValGluCy 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        558 gValAmpLeuLeuValGlyProGly---AlaAlaGlnAlaAlaIleLysGluAmpProTr 577
-- ProProGluGluGluLysAsn----- ProTyrLysGluVa 431
                                                                                      431 lTyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProProProAlaLy 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         577 pAsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgGluAspTr 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      466 ---IleIleAspGluArgThrArg-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    489 -----IleCysIleSerCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             528 yTyrGlnSerTyrCysThrIleCys------CysGly------
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STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2638 degactgatattacttctgtgactcttgggdatacaacagctgt-caaaaccaaaatact 2696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2877 GAGGGTTGCCAGCCTCCTAAAAAGGCCCAAAGCTCAGCTCTGCAAGATTGAGAAGAGTAA 2936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2464 AATAAGCGGGAGTCAAGGAAAGAGAAAAAGGAAAAAGGGATCAGAAATTCAGAGTAGTTCT 2523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 ArgSerGluProGlnProGluGluGlySerProAlaAlaGlyGlnLysGlyGlyAlaPro 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 ------GlualaSerArgAlaValGlu 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 AlaGluGlyGluGlyThrGluThrProPro---------------------------122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 GlyPro-----SerAspLeuLeuProAsnGlyAspLeuGluLys 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 SerSerSerSerLeuGluArgGluAspAspArgLysGluGlyGluGluGluGluAsn 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 AsnGlyCysCysValThrLysGluGlyArgGlyAla-----------
ZIP: 19103

CORPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PROFF COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
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                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca Eeq., Mark
REGISTRATION NUMBER: 33,229
REFERNICE/DOCKET NUMBER: TUU-1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Best Local Similarity:
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; ANTI-SENSE:
PCT-US94-04496-1
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DB:
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	DOTE TOWN	ç	
	ARE: FAC APPLICAT CATION NU G DATE:	CURRENT APPLI FILIN	, ., ., .,
	READABLE FORM: TYPE: Floppy disk RR: IBM PC compatible RR: SYSTEM: PC-DOS/MS-DOS		
		2100	
	ESPONDENCE ADDRESS DRESSEE: Arnold, REET: P. O. Box 4	CORR	
	OF INVENTION: DETECTING GENE REARRANGEM OF INVENTION: TRANSLOCATIONS R OF SEQUENCES: 8	TITLE TITLE	
	NERAL INFORMATION: APPLICANT: Rowley, Janet D. APPLICANT: Diaz, Manuel O. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR	GENERA APPI APPI TITL	
)-255-4 :e 4, Application US/08080255 No. 5487970	SULT 14 -08-080 Sequenc	· · · · · · · · · · · · · · · · · · ·
	GGATGCACAGTGGTCTCATGATTTCTCACTGTCATGAT 4488	4449	Db
		597	Š
444	GATCTGTACCAAGTGTGTTCGCTGTAAGAGCTGTGGATCCACAACTCCAGGCAAAAGGGTG	4389	Db
597	pAsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgGl	577	Ş
438	CCTGGGACCAAACTACCCCACCAAACCCACAAAGAAGAAGAAGTCTG	4341	Db
577	sValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLys	558	δδ
434	TACAAAGCAGCTGCTGGAGTGTAATAAGTGCCGAAACAGCTATCACCCTGAGTG	4287	d d
558	-GlyArgGluValL	539	δ.
428		4227	DЪ
538	yTyrGlnSerTyrCysThrIleCys	528	Ş
422		4167	d d
528	s	513	δõ
416	TGCCAGTAGTGGGCATGTAGAGTTTGTGTATTGCCAAGTCTG	4125	바
513	sGlySerLeuAsnValThrLeuGluHisProLeuPheIleGlyGlyMetCysGlnAsnCy	493	Ş
412	GGGAGGCTTAGGAATCTTGACTTCTGTTCCTATAACACCCAGGGTGGTTTGCTTTCTCTG	4065	aa
493		489	Q
406	::: GATCAGAGTGGACTTTAAGGAGGATTGTGAAGCAGAAAATGTGTGGGA	4005	đđ
488	GluArgLeuValTyrGluValArgGlnLysCysArgAsnIleGluAsp	473	Ş
400	: : : GAACATCCTCAGCACTCTCTCCAATGGCAATAGTTCTAAGCAAAAATTCCAGCAGATGG	3945	d d d
472	IleIleAspGluArgThrArg	466	ρ
394	:	3885	D)
465		459	Qy
388	AGGTCCAGAGCAGAGCAAACAGAAAAAAGTGGCTCCCCGCCCAAGTATCCCTGTAAAACA	3825	da

us-09-720-086-5.rni

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::: ||||:::||||:::||| 257 GCTGACAAGAGAAAAGAGAAGAGAGAGAGAGAAAAAGGAG 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 rAsnIleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTr 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 ThralaArgLysValGlyArgProGlyArgLysArg---LysHisProProValGluSer 59
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148
105
274
211
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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HATTORNEY/AGENT INFORMATION:

NAME: Parker, David L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: ARCD:072/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-7200
TELEPHONE: (512) 474-7577

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 4201 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
TYPE: MOLECULE TYPE: DNA (genomic)
US-08-080-255-4
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157.00
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Pred. No.:
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g	950GAAGA 966
ò	212 sLysAlaLysVallleAlaValMetAsnAlaValGluGluAsnGlnAlaSerGlyGluSe 232
Ωp	rgrerr
ò	232 rGlnLysValGluGluAlaSerProProAlaValGlnGlnGlnProThrAspProAlaSerPr 252
q	1025GAAGATGCTGAACCTCTTGCTCCACCCATCAAACCAATTAAACC 1068
ζ	252 oThrValAlaThrThrProGluProValGlyGlyAspAlaGlyAspLysAsnAlaThrLy 272
đ	1069 TGTCACTAGAAA 1080
ò	272 sAlaAlaAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeuVa 292
g	1081 CAAGGCACCCCAGGAACCTCCAGTAAAGAAAGGACGTCG-ATCGAGGCGGT 1130
ò	292 lTrpGlyLysLeuArgGlyPheSerTrpTrpFroGlyArglleValSerTrpTrpMetTh 312
d d	1131 GTGGGCAGTGTCCCGGCTGCCAGGTGCCTGAGGACTGTGGTGTTGTA 1178
ò	312 rGlyArgSerArgAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLysPh 332
q	1179 CTAATTGCTTAGATAAGCCCAAGTTTGGTGGTCGCAATATAAAGA 1223
ò	332 eSerValValCysValGluLysLeuMetProLeuSerSerPheCysSerAl 349
qq	
ò	349 aPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLysAlalleTyrGluValLe 369
đ	1284 ACCTGCAGAAGCTAAAGCTGTGAAA-AGAAAGAGAAAAAGTCTAAGACCAGTGAA 1342
ò	369 uGlnValAlaSerSerArgAla376
Ω	1343 AAGAAAGACAGCAAAGAGAGCAGTGTTGTGAAGAACGTGGTGGACTCTAGTCAGAAACCT 1402
ò	377GlyLygLeuPheProAlaCysHisAspSerAspGluSerAspSerGl 392
q	1403 ACCCCATCAGCAAGAGGGATCCTGCCCCAAAG-AAAAGCAGTAGTGAGCTCCTCCACG 1461
ò	392 yLysAlaValGluValGlnAsnLysGlnMetIleGluTrpAlaLeuGlyGlyPheGlnPr 412
οp	1462 AAAGCCCGTCGAGGAAAAGAGTGAAGAAGGGAATGTCTCGGC 1503
δŏ	412 oSerGlyProLysGlyLeuGluProProGluGluGluLysAsnProTyrLysGl 430
qq	1504 CCCTGGGCCTGAATCCAAACGGCCACCACTCCAGGTTCCAGGAAGTCAAGCAAG
ò	430 uValTyrThrAspMetTrpValGluProGluAlaAlaAlaAyrAlaProPro 447
g	1564 CTCCCAGCCAGCACTGGTCATCCCGCCTCAG
ò	448 -ProProAlaLysProArgLysSerThrThrGluLysProLysValLys 464
q	1609 ACCGCCAAGAAAGAAGTTCCCAAAACCACTCCTAGTGAGCCCAAGAAAAAGCAGCCTCC 1668
ò	465GluileileAspGluArgThrArgGluArgLeuValTy 477
q	1669 ACCACCAGAATCAGGTCCAGAGCAGAGCAAACAGAAAAAAAGGTGGCTCCCGGCCCAAGTAT 1728
δ	477 rGluValArgGlnLysCysArgAsnIleGluAspIleCysIleSe 492
엄	1729 CCCTGTAAAACAAAAACCAAAAGAAAAGGAAAAACCACCTCCGGTCAATAAGCAGGAGAA 1788
ò	492 rCysGlySerLeuAsnValThrLeuGlu
g	1789 TGCAGGCACTTTGAACATCCTCAGCACTCTCCAATGGCAATAGTTCTAAGCAAAAAT 1848

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; Patent No. 6121419
; GENERAL INFORMATION:
APPLICANT: Rowley, Ja
; APPLICANT: Diaz, Manu
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-08
                                                                                                 TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
           STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2191
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 1 FILING DATE: 06-JUN-: CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DETECTING GENE REARRANGEMENTS TITLE OF INVENTION: TRANSLOCATIONS
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                                                                                                                                                                    NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:072/PAR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/080,255
FILING DATE: 17 JUNE 1993
ATTORNBY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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STREET: F.
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Texas
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                                                           TYPE: nucleic acid
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                                                                                                                                                      TELEPHONE:
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                                                                                  4201 base pairs
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Diaz, Manuel O.
                                  linear
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oThrValAlaThrThrProGluProValGlyGlyAspAlaGlyAspLysAsnAlaThrLy 272
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                                                                  rGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAspProAlaSerPr 252
                                                                                                    ACGAGAAAAGATTTTGTCTTCCATGGGGAATGATGACAAGTCATCAATTGCTGGCTCA-- 1024
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ð	 	 GTGGTGTTTGTA 1178
ي ج	yy 312 rGlyArgSerArgAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLy8Ph in 1179 cmaammgcmmaGli [yAspGlyLysPh 332
>	332 eSerValValCysValGluLysLeuMet	
, α	1224 AGCAGTGCTGCAAGATGAGAAATGTCAGAATC	
> .	349 aPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLysAl	
Ω	1284	
۾ ج	y 369 ucinvalalaserseratgala	AGTCAGAAACCT 1402
>	y 377GlyLysLeuPheProAlaCysHisAspSerAspGluSerAspSerGl	userAspserGl 392
Ω	b 1403 acccatcagcaagagagatctgccccaaag-aaaagcagtagtgagcctcctccacg	GCCTCCTCCACG 1461
<u>~</u>	392 yLysAlaValGluValGlnAsnLysGlnMetIleGluTrpAlaLeuGly 	74
۵	1462 AAAGCCCGTCGAGGAAAAGAGTGAAGAAGGG	GAATGICTCGGC 1503
<u>></u>	y 412 oSerGlyProLysGlyLeuGluProProGluGluGluLysAsnProTyrLysGl	430
۵	1504	AAGCAAGCAGGT 1563
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Ω	1564 CTCCCAGCCAGCACTGGTCATCCCGCCTCAG	ACCTACTACAGG 1608
ع ح	448 -ProProAlaLysEysProArgLysSerThrThrGluLysProLy	8ValLys 464
>	465GlullelleAspGluArgThrArgGluArgLeuVal	y 477
Ω	1669 ACCACC	CCGCCCAAGTAT 1728
>	477 rGluValArgGlnLy	AspileCysileSe 492
Д	1729	TAAGCAGGAGAA 1788
>	492 rCysGlySerLeuAs	105 201
Ω	1789	TAAGCAAAAAT 1848
ح.	y 502HisProLeuPhelleGlyGlyMetCysGlnAsnC	tCysGlnAsnCy 513
Ω	1849	rrecchagrere 1908
>	y 513 gLygABnCyBPheLeuGluCyBAlaTyrGlnTyrAgpAspAgD	rAspAspAspGl 528
Q	1909 T	GGAGGACCAGCT 1968
>	y 528 yTyrGlnSerTyrCysThrIleCysCysGly	538
Q	1969 ggaaaattggtgttgtggttgcaaattgtgtggaa	AGGCAACATCAGGC 2028
>	GlyAsn	eCysValGluCy 558
ρ	b 2029 TACAAAGCAGCTGGTGGAGTGTAATAAGTGCCGAAACAGCTATCACCCTGAGT	rcaccerdadrd 2082

Search completed: November 25, 2002, 01:45:03 Job time : 312.239 secs

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OM nucleic - nucleic search, using sw model

Run on: November 22, 2002, 08:18:31; Search time 84.7727 Seconds (without alignments) 15175.990 Million cell updates/sec

Title: Perfect score:

Sequence:

Scoring table:

ned: 441362 segs, 153338381 residues

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

AT TE INFO SE	PR CG CS	RESULT US-09-2 Pacen Pacen GENE AP
AGENTION AGENTION Lynn E Lynn	NUMBER OF SEQUENCES: 134 CORRESPONDENCE ADDRESS: ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/276,531 FILING DATE: Herewith CLASSIFICATION DATA: APPLICATION UNMBER: 60/079,677 FRIOR APPLICATION DATA: APPLICATION UNMBER: 60/079,677 FILING DATE: March 27, 1998	1 276-531-47 276-531-47 ence 47, Application US/09276531 nt No. 6183968 ERAL INFORMATION: PPLICANT: Bandman, Olga PPLICANT: Hallman, Jennifer L. PPLICANT: Yue, Henry PPLICANT: Yue, Henry PPLICANT: Reddy, Roopa PPLICANT: Reddy, Roopa PPLICANT: Guegler, Karl J. PPLICANT: Guegler, Karl J. PPLICANT: Baughn, Mariah R. PPLICANT: Baughn, Mariah R. PPLICANT: TINENTION: COMPOSITION FOR THE DETECTION OF GENES ENCOUNTIES OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL
)ING PROLIFERATION

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                                                                                                            2295 GGCTCTTCTTCGAGTTTTACCACTTGCTGAATTATACCCGCCCCAAGGAGGGCGACAACC 2354
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                                          Ouery Match
Best Local Similarity 71.4%; Pred. No. 1.8e-144;
Matches 888; Conservative 0; Mismatches 306; Indels 49; Gaps
                                                                                                                                                                                                                                                                                                                                           244 ACAGGGCCCGATACTTCTGGGGCAACCTACCCGGGATGAACAGGCCCGTGATAGCATCAA 303
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                                                                                                                                                                                         1125 TCGTTTTTTCCCAGGGCAAGCAGAAG----AGAAAATGTTGTATATGTC----TTTACC 1176
                                                                                                                                                                                                                                                                                                   1253 GGAGAGTCACTGGAGGACCAGCTGAAGCCCATGCTGGAGTGGGCCCACGGTGGCTTCAAG 1312
                                                3301 CATTIGCTGGAGGATGCTATTGTGAATGTGGGCTCAGATGAGCAAGGTCAAGGGGGCCAAA 3360
                                                                                                 1065 retritacadacererecaerreragecareraegeracadaearrirraaggeeeeaga 1124
                                                                                                                                                                                                                                                              3421 TGGCACCTTCCCCTTGCTTTGGTACAAGGCTGAAGTCCTGTTGG-----TCTTGTAG 3473
1018 G-----ACAGTTATTGCAAGAGTTTAATTTTTGAAAACTGGCTACTGCTCTG 1064
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                                                                                                                                                                                                                                                                                                                                                                        3474 CATTTCCCAGGATGATGATGTCAGCAGGGATGACATCACCACC 3516
                                                                                                                                                                                                                                                                                                                                                                                                                1237 TTTCCACAATGATGATTTTCAGCAGGATGACGTCATCATC 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE:
CLANCOLORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-222-463-14/C
'Sequence 14, Application US/08232463
'Sequence 14, Application US/08232463
'Fatent No. 5670367
'SENERAL INFORMATION:
'APPLICANT: DONNER, F.
'APPLICANT: SCHEIFLINGER, F.
'APPLICANT: SCHEIFLINGER, F.
'APPLICANT: FALKNER, F. G.
'TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS'
'NUMBER OF SEQUENCES: 5.
'ADDRESSER: Foley & Lardner'
'STREET: 1800 Diagonal Road, Suite 500
'CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30472/114 IMMU
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CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/07/935,313
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAMME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
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INFRMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC COMPA
OPERATING SYSTEM: PC-D
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IMMEDIATE SOURCE:
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GENERAL INFORMATION:
                                                                                                                     TELEX: 899149
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           ZIP: 22313-0299
OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vo
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1613
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TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                     LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE FOR THE FIRST STATE 
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linear
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; CLONE: pTZgpt-F1s
US-08-232-463-14
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                                                                                                                             US-09-333-423-1
                                                                                                                                                                                                                                             SEQ ID NO 1
                                                                            Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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APPLICANT: Thelen, Jay
APPLICANT: Miernyk, Jan
                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 1999-06-15
EARLIER APPLICATION NUMBER: 60/089,998
EARLIER FILING DATE: 1998-06-19
                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 0818
CURRENT APPLICATION NUMBER: US/09/333,423
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Pyruvate Dehydrogenase Kinase TITLE OF INVENTION: Polynucleotides, Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Muszynski, Michael APPLICANT: Sewalt, Vincent
                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version
                                                                                                                                        ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (55)...(1095)
                                                                                                                                                                                                             TYPE: DNA
                              3128 GATGGCTTTCTTTTACCCTCCTGAGTTTTATCACTCAGAAGTGATGGCTAAGATACCAAAA 3187
                                                                                                                                                                                                                             ENGTH: 1332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGAGTCACCCCTGCCTGAAGGCACCTCACCTGTCCCCTTTTTAGCTCACCTGTGTGGG 2948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.1%; Score 45.2; DB 1; nilarity 4.3%; Pred. No. 0.035; Conservative 212; Mismatches 165;
                                                               Conservative
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                                                                            65.6%;
                                                             0
                                                                            Score 43.2; DB 4;
Pred. No. 0.047;
                                                             Mismatches
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                                                                                           Length 1332;
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APPLICANT: De Greef, willy
APPLICANT: Van Emmelo, John
APPLICANT: Van Emmelo, John
APPLICANT: De Oliveria, Dulce E.
APPLICANT: De Souza, Maria-Helena
APPLICANT: Van Montagu, Marc
TITLE OF INVENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS OR
TITLE OF INVENTION: EMBRYOS
                                                                                                                                                                                                                              COMPESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: BOX 1404
CITY: D. BOX 1404
CITY: D. BOX 1404
CITY: United States
ZIP: 22313-1404
COMPUTRY: United States
ZIP: 22313-1404
COMPUTRY: LIBM PC COMPALIB
COMPUTRY: ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRY: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRY: BEADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTRY: BOX 1806
SOPERATING SYSTEM: PC-DOS/MS-DOS
SOPERATING SYSTEM: DATA:
APPLICATION NUMBER: US/08/361,467B
FILING DATE: 2-DEC-1994
CLASSIFICATION NUMBER: US/08/361,467B
FILING DATE: 04-APR-1991
RADELICATION NUMBER: WO PCT/EP90/01275
FILING DATE: 01-AUG-1999
RATOR APPLICATION NUMBER: EP 89 402 224.3
FILING DATE: 01-AUG-1989
ATTORNEY/AGENT INFORMATION:
NUMBE: SCAULMAN; BA-C6620
FILING DATE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1046 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3194 ACAAAAACAGAAACAAAAAAAAAAA 3221
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nucleic acid
EDNESS: double
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MOLECULE TYPE: CDNA

I IMMEDIATE SOURCE:

CLONE: 3C9

US-08-361-4678-4
Patent No. 5633441
GENERAL INFORMATION:
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US-08-484-332C-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.0%; Score 42.8; DB 4; Length 812; Best Local Similarity 61.8%; Pred. No. 0.046; Matches 68; Conservative 0; Mismatches 42; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       674 TAGACACGTTCGGTTTTTTTTTTCTCCGTAGCTTCGCAATGACTGCCCACGCTAAAAA 733
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APPLICANT: TAKESAKO, KAZUTOH
APPLICANT: TAGEHARA, TOMOKO
APPLICANT: YAGTHARA, TOMOKO
APPLICANT: VORDH, WASANOBU
APPLICANT: KATOA, RUNOSHIN
APPLICANT: KATO, IKUNOSHIN
APPLICANT: KATO, IKUNOSHIN
APPLICANT: TAMOKO, HINOSHI
APPLICANT: YASUBDA, HIROSHI
APPLICANT: YAMGUCHI, HIDEYO
TITLE OF INVENTION: ANTIGENIC PROTEIN ORGINATING IN
TITLE OF INVENTION: AMAGSEZIA
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CARRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,097
FILING DATE:
3188 AAACAAACAAAACAGAAACAAAAAAAAAAAAA 3223
                               1296 AANAAAAAAAAAAAAAAAAAAAAAAAAAA 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0346P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
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US-08-361-467B-4
; Sequence 4, Application US/08361467B
                                                                                                                       RESULT 5
US-09-091-097-7
Sequence 7, Application US/09091097
Patent No. 6432407
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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; LOCATION: 2..673
US-09-091-097-7
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889 CGTAGTTTTCTTGTTTTTCCTATTTTGTTTCTCTCTATCAAAACCCAACAGTAAAATGGA 948
                                                       0; Gaps
Query Match
1.0%; Score 42.4; DB 1; Length 1046;
Best Local Similarity 55.4%; Pred. No. 0.069;
Matches 82; Conservative 0; Mismatches 66; Indels 0
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/361,467
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                              3194 АСАЛАЛАСАGAЛАСЛАЛАЛАСЛАЛАЛА 3221
                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
CLONE: 3C9
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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TITLE OF INVENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS
                                                                                                                                689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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REFERENCE/DOCKET NUMBER: 010830-093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1036
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                                                                                                                             CGTAGTTTTCTTGTTTTCCTATTTTGTTTCTCTCTATCAAAAACCCAACAAGTAAAATGGA 948
                                                              INFORMATION:
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P.O. Box 1404
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De Oliveria, Dulce E.
De Souza, Maria-Helena
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                                                                                                                                                                                               0; Mismatches
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US-09-196-390-1
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                 Query Match
Best Local
      Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                    TOPOLOGY: Illear
MOLECULE TYPE: CDN
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 28-MAY-
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PRIOR APPLICATION NUMBER: DE 196 21 588.9
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                                                                                                                                                                     HAPLOTYPE: ca.
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2239 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 29-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 1
FILING DATE: 11-SEP-1996
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TITLE OF INVENTION:
                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 596-9000
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                                                                                                                                                                                                                                                      ANTI-SENSE: NO
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                                                                                     NAME/KEY:
LOCATION:
                                                                                                                                   CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Haley, Jr., James F REGISTRATION NUMBER: 27,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/196,390
                                                                                                                                                        LIBRARY:
                                                                                                                                                                                                       STRAIN:
                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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    86;
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                     Similarity
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                                                                                                                                                                                                       CV.
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      Conservative
                                                                                                                                                     cDNA library in pBluescript sk (-)
                                                                                                                                                                                                                                                                                                                                                                                                         (212) 596-9090
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Kossmann, Jens
KOSSMANN, Jens
VENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
VENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH
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Walter, Lennart
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                   54.1%;
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                 Score 42.2; DB 4; Length 2239; Pred. No. 0.12;
      Mismatches
73;
    Indels
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   Gaps
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EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-06-25
EARLIER FILING DATE: 1997-06-25
EARLIER FILING DATE: 1997-06-25
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-06-2
                 FILING DATE: 1997-05-23
2042 GCCTTCTGTGTGTTGTCTTTGTCCTTAGCTGACAATATTTGACCTGTTGGAGAATTTT 2101
                                                                                               3133 CITICITITACCCTCCTGAGTTTATCACTCAGAAGTGATGGCTAAGATACCAAAAAACA 3192
                                                                                                                                                               2102 ATCTTTGCTGCTGTTTTTTTTATCAAAAGAGGGGGTTTCCTCCGATTTCATTAAAAA 2161
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GENERAL INFORMATION:

APPLICANT. ROSEN et al.

TITLE OF INVENTION: 186 Human Secreted proteins
FILE REPRENCE: P2002P1

CURRENT APPLICATION NUMBER: US/09/149,476

CURRENT PILING DATE: 1998-09-06

EARLIER PILING DATE: 1998-03-06

EARLIER PILING DATE: 1997-03-07

EARLIER PILING DATE: 1997-03-07

EARLIER PILING DATE: 1997-03-07

EARLIER PILING DATE: 1997-03-07

EARLIER PELING DATE: 1997-03-07

EARLIER PELING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,334

EARLIER APPLICATION NUMBER: 60/040,336

EARLIER APPLICATION NUMBER: 60/040,336

EARLIER APPLICATION NUMBER: 60/040,336

EARLIER APPLICATION NUMBER: 60/040,336

EARLIER APPLICATION NUMBER: 60/040,502

EARLIER APPLICATION NUMBER: 60/040,502

EARLIER APPLICATION NUMBER: 60/040,503

EARLIER PELING DATE: 1997-05-23

EARLIER PELING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/040,503

EARLIER PELING DATE: 1997-05-23

EARLIER 
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18-09-149-476-208
Sequence 208, Application US/09149476
Perent No. 6420526
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ER APPLICATION NUMBER: 60/056,887
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,908
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/048,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,614
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/043,578
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,576
ER FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,594
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,589
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,593
                                           R FILING DATE:
R APPLICATION N
FILING DATE:
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FILING DATE: 1997-09
APPLICATION NUMBER:
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,875
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,881
FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
                                                                                         FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/057,669
FILING DATE: 1997-09-05
APPLICATION NUMBER: 60/049,610
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/056,862
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/047,599
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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                                            NUMBER: 60/
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LIER APPLICATION NUMBER: 60/056,862
LIER APPLICATION NUMBER: 60/056,887
LIER APPLICATION NUMBER: 60/056,987
LIER FILING DATE: 1997-08-22
LIER APPLICATION NUMBER: 60/056,908
LIER FILING DATE: 1997-08-22
LIER APPLICATION NUMBER: 60/057,650
LIER APPLICATION NUMBER: 60/057,650
LIER APPLICATION NUMBER: 60/057,669
LIER APPLICATION NUMBER: 60/057,669
LIER APPLICATION NUMBER: 60/057,669
LIER APPLICATION NUMBER: 60/057,669
LIER APPLICATION NUMBER: 60/049,610
LIER APPLICATION NUMBER: 60/049,610
LIER FILING DATE: 1997-06-13
LIER APPLICATION NUMBER: 60/061,060
LIER FILING DATE: 1997-10-02

V Match
Local Similarity 60.5%; Pred. No. 0.11;
hes 69; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

밁 Ś CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,621
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER APPLICATION NUMBER: 60/040,163 US-09-149-476-24 Patent No. EARLIER
EARLIER EARLIER EARLIER TITLE OF INVENTION: 186
FILE REFERENCE: PZ002P1 3118 INFORMATION TAGGTAGTAAGATGGCTTTCTTTTACCCTCCTGAGTTTATCACTCAGAAGTGATGGCTAA 3177 APPLICATION I APPLICATION NUMBER: 6 FILING DATE: 1997-05-24, Application o. 6420526 APPLICATION FILING DATE: APPLICATION FILING DATE: APPLICATION FILING DATE: APPLICATION I FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/ APPLICATION NUMBER: APPLICATION NUMBER: 6 FILING DATE: 1997-05-APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION APPLICATION FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1997-05-FILING DATE: APPLICATION FILING APPLICATION FILING DATE FILING DATE FILING DATE: FILING DATE: 1997-05-23 FILING DATE: FILING DATE Rosen DATE: NUMBER: 6 NUMBER: 6 NUMBER: NUMBER: NUMBER: NUMBER: NUMBER: NUMBER: NUMBER: NUMBER: 1997-05-1997-05-1997-05-1997-05-1997-05-1997-05-1997-05-1997-05-1997-05-23 1997-05-1997-05-23 US/09149476 Human Secreted proteins 60/047,582 60/047,492 60/047,587 60/047,581 60/047,592 60/047,503 60/047,618 60/047,617 60/047,583 60/047,633 60/047,502 60/047,615 60/047,600 60/047,613 60/047,598 60/047,500 60/047,584 60/047,597 3231 . 1307

APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-05-23

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Page 8

0; Gaps ch 1.0%; Score 42; DB 4; Length 2323; l Similarity 60.5%; Pred. No. 0.14; 69; Conservative 0; Mismatches 45; Indels EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/05,761
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-23
EARLIER FILING DATE: 1997-08-23
EARLIER FILING DATE: 1997-08-23
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
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EARLIER APPLICATION NUMBER: 60/047,586
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-06-23
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-06-23
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EARLIER FILING DATE: 1997-06-23
EARLIER FILING Query Match Best Local Matches 6 g ઠે

ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,632
ER APPLICATION NUMBER: 60/043,580
ER APPLICATION NUMBER: 60/043,580
ER APPLICATION NUMBER: 60/043,580
ER FILING DATE: 1997-04-11
ER FILING DATE: 1997-04-11
ER FILING DATE: 1997-04-11
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,569
ER APPLICATION NUMBER: 60/043,311
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,671
ER APPLICATION NUMBER: 60/043,671
ER APPLICATION NUMBER: 60/043,671
ER APPLICATION NUMBER: 60/043,671
ER APPLICATION NUMBER: 60/043,672
ER APPLICATION NUMBER: 60/043,672
ER APPLICATION NUMBER: 60/043,673
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,313
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,672
ER APPLICATION NUMBER: 60/043,313
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,313
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/066,873
ER FILING DATE: 1997-06-22
ER APPLICATION NUMBER: 60/056,873
ER FILING DATE: 1997-06-22
ER APPLICATION NUMBER: 60/056,911
ER APPLICATION NUMBER: 60/056,9

3118 TAGGTAGTAAGATGGCTTTCTTTTACCCTCCTGAGTTTATCACTCAGAAGTGATGGCTAA 3177

APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,864 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,631

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RESULT 11
US-08-731-272A-29/c
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Best Local S
Matches 61
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TELEFAX: (202) 293-7060
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Apprin
Sequence 5, Application US/09370473
Patent No. 6271031
GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Layo O.
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-43086
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP HEI.
FILING DATE: 17-CCT-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NUCLEIC ACID OF C TYPE HEPATITIS VIRUS USING TITLE OF INVENTION: DERIVATION AND PROCESS FOR DETECTION VIRUS USING TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tanaka, Torahiko
APPLICANT: Katoh, No. 5837463uyuki
APPLICANT: Shimotohno, Kunitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION,
                                                                                                                                                                                                                       145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCTCAACAGCTCTCTTAGTACTCAGGTTCATG 3255
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                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
LENGTH: 2091
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: GONG, FANGCHENG et al
TITLE OF INVENTION: ISOLATED HUMAN CASEIN KINASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN CASEIN KINASE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Office 97 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09813818
Patent No. 6448057
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CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: 60/096,240
EARLIER FILING DATE: August 12, 1998
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Quinolinate Metabolism
FILE REFERENCE: BB-1209
                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/813,818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                          ORGANISM: Human
                                                                                                                                                                                                                                                                                        TYPE: DNA
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2041
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                                                                                                                                                           3197
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les 81; Conserv
                             CAAACAAAAACAGAAACAAAAAACAAAAAAAAAACCTCAACA 3231
                                                                                            GGCTTTCTTTTACCCTCCTGAGTTTATCACTCAGAAGTGATGGCTAAGATACCAAAAAAA 3190
                                                                                                                           CCGCCCTGTACTCCCTGACGATTCCACTGTAACTACCAATCTTCTACTTGGT--TAAGAC 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARAAAAAAAAAAAAAAAAAAAAAAA 1871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAACAGAAACAAAAACAAAAAAAA 3223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   СТТТТАСССТССТВАСТТАТСАСТСАВЛАВТВАТВЕСТАЛВАТАССАЛАЛАЛАВСАЛАСА 3196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTGTGGCTGGAATCATGTTCTGATATTTCAGATGTATAGGACAGCAGATGATTTGTACT 1784
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                                                             Similarity
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Pred. No. 0.2;
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RESULT 14 US-08-50-67BA-30/c : Sequence 30, Application US/08520678A ; Patent No. 5874565 ŧ

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Search completed: November 22, 2002, 09:19:58 Job time : 212.773 secs
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Barent No. 6297003
GENERAL INFORMATION:
APPLICANT: Rice, Charles M.
APPLICANT: Rice, Charles M.
APPLICANT: Rolykhalov, Alexander A.
TITLE OF INVENTION: VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 FORSYth Blvd., Suite 1400
GENERAL INFORMATION:
APPLICANT: Rice, Charles M.
APPLICANT: Rice, Charles M.
APPLICANT: ROJVKHOLOV, Alexander A.
APPLICANT: KOJYKHOLOV, ALEXANDER A.
TITLE OF INVENTION: CVIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 FORSYTH Blvd., Suite 1400
CITY: St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.0%; Score 40.8; DB 2; Length 270;
Best Local Similarity 67.9%; Pred. No. 0.088;
Matches 57; Conservative 0; Mismatches 27; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,678A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6029-6836
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COUNTRY: USA
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPBERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFTCATION: 536
ATTORNEY, AGENT INFORMATION:
NAME: Henderson, Melodie W.
REGISTRATION UNMERS: 37,848
REFERENCE/DOCKET NUMBER: 6029
TELECOMMUNICATION INFORMATION:
TELEFAX: 314-727-5188
TELEFAX: 314-727-6092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INPORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-678A-30
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US-08-897-126-30/c
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0; Gaps
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1.0%; Score 40.8; DB 4; Length 270;
Best Local Similarity 67.9%; Pred. No. 0.088;
Matches 57; Conservative 0; Mismatches 27; Indels (
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,126
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520,678
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Henderson, Melodie W.
REGISTRATION NUMBER: 37,848
REFERENCE/DOCKET NUMBER: 6029-6836
TELEPHONE: 314-727-5188
TELEPHONE: 314-727-5092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OY 3236 TCTTAGTACTCAGGTTCATGCTGC 3259
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-897-126-30
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 s
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-Q=/cgn2_1/USPTO_spool/US09720086/runat_18112002_092957_29457/app_query.fasta_1.4252
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=humanf0.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=200000000
-USER=US09720086_@CGN 1_1_108_@runat_18112002_092957_29457 -NCPU=6 -ICPU=3
-NO XLPXY -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
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Match
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4566
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     Copyright
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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    2077
6328
6328
2352
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3421
4481
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 US-09-276-531-47

US-08-913-832A-1

US-09-249-181A-1

US-08-913-159-12

US-09-484-970B-8

US-09-041-886-18

US-09-105-537-5

US-09-120-878-19

US-09-320-878-19

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US-08-923-137-1

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Sequence 1, Appli	۱.,	equence 5	ወ	ø	•	L	O	Ce	\vdash	1	4	Ļ	σ	\mathbf{H}		\vdash	w	\vdash	4	\vdash	\mathbf{L}	ø	w	-	Çī	1, Appl	34, App	29,	: 29, App	29, App	54	-

ALIGNMENTS

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GENERAL INFORMATION:
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                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: COMPOSITION FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                 CITY:
STATE:
                            APPLICATION NUMBER: 60/079,677
FILING DATE: March 27, 1998
                                                                                FILING DATE: H
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                STREET:
                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                 ZIP: 94304
                                                                                                                                                                                                                                                 COUNTRY:
                 CLASSIFICATION:
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CALIFORNIA
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Hillman, Jennifer L.
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Baughn, Mariah R.
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                                                                                              Herewith
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728 AlaAlaHisArgAlaArgTyrPheTrpGlyAsnLeuProGlyMetAsnArgProVallle 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AGG---CGGCTCTTCTTCGAATTTTC-CACCTGCTGAATTACTCACGCCCCAAGGAGGGT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeulyglysValGlnThr1leThrThrLygSerAsnSer11eLysGlnGlyLygAsnGln 787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  668 ThrGlyArgLeuPhePheGluPheTyrHisLeuLeuAsnTyrSerArgProLysGluGly 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 GATGACCGGNCGTTCTTCTGGATGTTTGAGAATGTTGTAGNCTCGTGCCGATTCGGCAGA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            708 ArgAspileSerArgPheLeuGluCysAsnProValMetileAspAlaileLysValSer 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357 TTAAAGAAAGTACAGACAATAACCACCAAGTCGAACTCGATCAAACAGGGGAAAAACCAA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 CTTTTCCCTGTTGTCATGAATGCAAGAAGATGTTTNGTGGTGCACTGAGCTCGAAAGG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GCCGGCNANTGCAACGATCTNNA-AATGTGAATCA-GCCAGGAAAGGCTGTATGAGGGAC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 GGGGACATCTCACGGTTCCTGGAGTGTAATCCAGTGATGATGATGCCATCAAAGTTTCT
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183
1
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-720-086-8 (1-853) x US-09-276-531-47 (1-2077)
NAME: Lyun E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REGISTRATION TOWNER: 42,918
REFRENCE/CONCENTRY
TELEPHONE: (650) 855-055
TELEPHONE: (650) 855-055
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2077 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                3,45e-76
903.00
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IMMEDIATE SOURCE:
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APPLICANT: Renz, Manfred
FILER REPERENCE: 8484-0030-999
CURRENT APPLICATION NUMBER: US/08/913,832A
CURRENT FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: PCT/DE96/00444
PRIOR FILING DATE: 1996-03-08
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
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SEQ ID NO 1
LENGTH: 6328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/249,181A CURRENT FILING DATE: 199-02-12 PRIOR APPLICATION NUMBER: US 08/913,832 PRIOR FILING DATE: 1998-01-12 PRIOR APPLICATION NUMBER: PCT/DE96/00444 PRIOR FILING DATE: 1996-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Seelig, Hans Peter
APPLICANT: Renz, Manfred
TITLE OF INVENTION: DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 8484-0059-999
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                                 ProProSerSerTyrLeuThrIleAspLeuThrAspAspThrGluAspThrHisGlyThr 180
                                                                                                                                                                                                                                                 ProAlaValArgThrArgAsnAsnAsnSerValSerSerArgGluArgHisArgProSer
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                                                                                                     {\tt ProAlaThrArgSerLeuArgArgAlaThrAlaSerAlaGlyThrProTrpProSer}
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                                                                                                                                           CCTAAGAAAGAGAAGAAGCAAATCCAAGCGGAAGGAGGAGGAG----
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Matches:
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/standard_name= "Gene coding for R.LlabII"
/label= r-llabII
/note= The first ten amino acids in this sequence may be doubtful. However, from base 773 this reading frame gives a homology with the Bsp6I endonuclease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEATURE:
NAME/KEY:
CONTION: 1392.2342
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /codon start= 1392
OTHER INFORMATION: /gone= "CRF"
OTHER INFORMATION: /gone= "CRF"
OTHER INFORMATION: /gone= "CRF"
OTHER INFORMATION: /donno== "Gene coding for M.LlaDII"
OTHER INFORMATION: /label= m-llaDII
OTHER INFORMATION: /label= m-llaDII
OTHER INFORMATION: /label= m-llaDII
OTHER INFORMATION: /noce= "The sequence shows 60 % identity and 76 % similarity
OTHER INFORMATION: /note= "The Bsp61 methylase."
                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Plasmid-derived type II
TITLE OF INVENTION: restriction-modification systems from Lactococcus lacis
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/08/913,159
FILING DATE:
                                                 1234 CCACACTGCGAGAAGGCATCCAGTGGGAAGCTAAAGAGGACAATTCGGAGGGTGAG 1293
525 TyrMetCysLeuProGln-ArgCysHisGlyValLeuArgArg------Ar 539
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/codon_start= 744
/product= "LlaDII restriction endonuclease"
/gence= EXPERIMENTAL
/gene= "ORF"
/number= 1
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PRINTED DATE:
PRINTED DATE:
PRILING DATE: 17-FEB-1995
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2355 base pairs
TYPE: nucleic acid
STRANDEDRESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
STRAINS: Lactococcus lactis subsp. cremoris
STRAIN: W39
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Matches:
Conservative:
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Patent No. 6300109
GENERAL INFORMATION:
APPLICANT:
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LOCATION: 744..1283
IDENTIFICATION METHOD:
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                            GlyArgSerTrpSerValProValIleArgHisLeuPheAlaProLeuLysAsp 848
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GGAAACAGTGTTGTAGTACCAGTTATAGAAAGAATTGCAAAAAATCTTGCAGAT
                                                                    TTCCCAAAAGAATAT---AAACTTCCAÁACCAAAGTAATGGGAGATTATATAAACAAGCA
                                                                                                                                             CTTACATATAGCGGAGATATTCGTAAATTAACACCAAGAGAATGCTTTAACGTTCAAGGT
                                                                                                                                                                            MetAsnGlyLysGluAspValLeuTrpCysThrGluLeuGlu-----ArgIlePheGly
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CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 8
LENGTH: 3522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING
FILE REFERENCE: PB-0014 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Incyte NAME/KEY: unsure LOCATION: 656, 658, 663 OTHER INFORMATION: a, t, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
1186 GAGGTCAACACCCAGGCCTACTGGAACTCCCTTGGAGAGAATAGAGACAGATATAAAGCA 1245
                                                                                                                                                                                  145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              766 ACAGACCAATCCACCCAAGAACCTTTCACAACTAAGATTCCACGAACAACTGAACTA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnAspLeuThrGlyAspGlyAspGlyGluAspGlyAspGlySerAspThrProValMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerAspGlnSerSerAspSerProProIleLeuGluAlaIleArgThrProGluIleArg
                                                                                                                                                                                                                                                        ArgGlnGlyArgAsnHisValAspGluSer---ProValGluPheProAlaThrArg--- 144
                                                                                                                                                                                                                                                                                                                             AsnAsnAsnSerValSerSerArgGluArgHisArgProSerProArgSerThrArgGly 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyArgArgSerSerSerArgLeuSerLysArgGluValSerSerLeuLeuSerTyrThr
                                                                                                                                                                                                                                                                                                                                                                                                        ProLysLeuPheArgGluThrArgThrArgSerGluSerProAlaValArg---ThrArg
                                 rHisGlyThrProGlnSerSerSerThrProTyrAlaArgLeuAlaGlnAspSerGlnGl 197
                                                                       ACTGGAAAGCCAGGAAGTGCAGGAATCATTTCATCAGGGCCCAATAACTACACCACCCCT
                                                                                                                                            CCACCCTTGCCACCCAGACCTACACACCCACGAAGAAAACCTTTACCACCAAATAATGTC
                                                                                                                                                                              ---SerLeuArgArgAlaThrAlaSerAlaGlyThrProTrpPro------
                                                                                                                                                                                                                      GCTGATAGAAATGTATCAGTGGACTCTACCCACCCACTAAAAAGCCAGGGACTCGCCGC
                                                                                                                                                                                                                                                                                             AGTGGGAATGGAGTGGGAACAGGGGTCAAGCAAGCACCCAGGCCA-----TCAGGT 1005
                                                                                                                                                                                                                                                                                                                                                                    AGACCTGTTCTGAATAGGACAACTACAAGACCTACTAGGCCCAAACCCAGTGGGATGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GCAAAGACAACTCAGGCGCCACACAGATTTTATACTACTGTGAGGCCCAGAACA
                                                                                                       ---SerProProSerSerTyrLeuThrIleAspLeuThrAspAsp-ThrGluAspTh 177
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2214 PACAPAPATICATTGAPATACTATGCGCATTCATTTAPAGCTATTTTGTTTACTATGTA 2273
                                                                                                                                                                    2274 TAAAAGTCTACAATTAATTAATAGCAATACTAGATGTTTATTATTAGAAAAGATTGCTG 2333
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|1375 GAAGAAATTATGGT-------GTAGTGTCTACGTATGATAGCAGTTTA 1416
                                                                                                                                                                                                                                                                                                                                                                   2334 AGAGTATTTATCAGGTTTTACAAAGTCCATTTTAAGAAAGCAAGATACTGATGTTAACAG 2393
                                                                                                                                                                                                                                                                                                                                                                                                                                              504 euGluVal------AlaAlaJyThrGlyThr-------AlaAlaG 515
                                                                                                                                                                                                                                                                                   11 GluGluAspAlaGlyGlyArgGluAspSerIleLeuValAsnGlyAlaCysSerAspGln 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Campbell & Flores Lip
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PID PC COMPUTER: PARTE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
FI
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 91,015
RELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SEG ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 4481 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: single
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; LOCATION: 163..4099
US-09-041-886-18
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Query Match:
DB:
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LeuPheSerGlnHisPheAsnLeuAlaThrPheAsnLysLeuVa 	282 2315	•
GlyLysPheSerGluValSerAlaAspLysLeuVal	267 2255	•
PheGlyAspGGGTTCCAAGACTAAGACCCAGGTCTC	264 2195	•
TrpLysAlaThrSerLysArgGlnAlaMetSerGlyMetArgTrpValGlnTrp- ::: :::::	246 2136	• •
GAGGGGTTCCATATCCAGTGGCCTAGAATTTGTATCCCACAA	239 2076	
AspGlyLysGluPheGlyIleGlyAspLeuValTrpGlyLysIleLysGlyPheSer'	219	
AlaAspSerGlyAspGlyAspSerSerGluTyr	207 1956	\
ProTyrAlaArgLeuAlaGlnAspSerGlnGlnGlyGlyMetGluSerProGlnValGlu	187 1899	
ThrIleAspLeuThrAspAspThrGluAspThrHisGlyThrPr	167 1861	
CCCATO	155	
AC :	151 1744	
al	131 1699	
ValSerSerArgGluArgHisArgProSerProArgSerThrArgGly:::	111	
PheArgGluThrArgThrArgSerGluSerProAlaValArgThrArgAsnAsnAsnS:::	91 1582	\
ThrGlyAspGlyAspGlyGluAspGlyAspGlySerAspThrProValMeter	71 1534	
SerSerSerArgLeuSerLysArgGluValSerSerLeuLeuSerTyrT::::	51 1474	
SerSerAspSerProProlleLeuGluAlaIleArgThrProGluIleArgGlyArgArg	31 1417	
7 O 1 H-0 20 1 20 - 20 20 1 O 0 0 H H O 1 O 1 O 1 O 20 20 H O 20 20 - K O 20 20 - K O 20 20 20 - K	CCCTGGCCATTCCAACTTCAACTTCAACTTCCAACTTCCAACTTCCAAACTTCCAAACCTTCAACTTCCAAACTTCCAAACTTCCAACTTCCAACTTCAACTTCAACTTCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAAACTTCCAAACTTCCAAACTTCCAAACTTCCAAACTTCCAAACTTCCAAACTTCCAAACTTCCAAACTTCCAAACTTCCAAACTTCCAAACTTCCAAAACTTCCAAAACTTCCAAAACTTCCAAAACTTCCAAAACTTCCAAAACTTCCAAAACTTCCAAAACTTCCAAAACTTCCAAAACTTCCAAAACTTCCAAAACTTCCAAAACTTCCAAAAACTTCCAAAAAA	31 SerSerAspSerProProIleLeu 417 TCTTCGTTATACAGTGCCCTTA 51 SerSerSerArgLeuSerLysArg 51 SerSerSerArgLeuSerLysArg 51 ThrGlyAspGlyAspGlyGluAsp 634 GCCCTGGAAAATGATGATGATAGAGAT 71 ThrGlyAspGlyAspGlyGluAsp 91 PheArgGluThrArgThrArgSer 91 PheArgGluThrArgThrArgSer 91 PheArgGluThrArgThrArgSer 91 PheArgGluThrArgThrArgSer 91 PheArgGluThrArgThrArgHisArg 131 AsnHisValAspGluSerProVal 132 ATTCCTCCTGGACAAGAAATAAAA 131 AsnHisValAspGluSerProVal 132 CCGCGTATGGGCCATCGCCTTGAC 133 ASTTCCTCACACTTCAGATTTCAAC 134 ACTTCTCACACTTCAGATTTCAAC 135 GlyThrProTrpProSer 14 ACTTCTCACACTTCAGATTTCAAC 155 GlyThrProTrpProSer 167 ThrIleAspLeuThrAspAspThr 167 ThrIleAspLeuThrAspAspThr 167 ThrIleAspLeuThrAspGlyAspSer 167 ThrIleAspSerGlyAspGlyAspSer 167 ThrIleAspSerGlyAspGlyAspSer 168 CTCTGCTCAAGGATGCCCCAAAGGC 167 AlaAspSerGlyAspGlyAspSer 168 GCCTCCAAGGATTCCAGTGGCCT 169 GGGTTCCAAGATTATCCAGTGGCCT 170 AspGlyLysGluPheGlyIleGly 171 AspGlyLysGluPheGlyIleGly 172 GAGGGGTTCCAAGATTATCCAGTGGCCT 173 GGGTTCCAAGATTATCCCCTAAAA 175 GGGTTCCAAGATTATCCCCTAAAA 175 GGGTTCCAAGATTATCCCCTAAAA 176 GGGTTCCAAGATTATCCCCTAAAA 177 GGGGTTCCAAGATTATCCCCTAAAA 177 GGGGTTCCAAGATTATCCCCTAAAA 178 GGGTTCCAAGATTATCCCCTAAAA 179 GGTTCCAAGATTATTCCCCTAAAA

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US-09-105-537-5/c
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Patent No. 6265202
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, Y.
APPLICANT: Zhao, L.
TITLE DEFERENCE: COO Against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
                                                                                                                                                                                                 31747 GGGCGTGTGGGGGGGTGGTGCGCGGGATGCG------CGGGGTGCGGCGCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 36778
TYPE: DNA
                                                      31642 GCCTCGGCGTCCAGG
                                                                                                                          31696 GCAGGACCGCGGTCGGGTCAGGTGTTACGGGGGCCGAGAGCC-----ATCCGGATCAGG
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                                                                                                                                                            30 GlnSerSerAspSerProProIleLeuGluAlaIleArgThrProGluIleArgGlyArg 49
                                                                                                                                                                                                                         10 GlyGluGluAspAlaGlyGlyArgGluAspSerIleLeuValAsnGlyAlaCysSerAsp
70 LeuThrGlyAspGlyAspGly----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyLysAspArgGlyAspGluAspGlnSerArgGluGlnMetAlaSerAspValAlaAsn 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaProLysArg----------LeuLysThrAsnCysTyrAsnAsn 406
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                                                                                ArgSerSerSerArgLeuSerLysArgGluValSerSerLeuLeuSerTyrThrGlnAsp
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30754 -CAGACCCCGGCGTTCGAGGAGTA-GAGGACGAAGGCGTCCAGCGGAGTGCCGCGGAGCA 30697
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399 uLysThrAsnCysTyrAsnAsnGlyLysAspArgGlyAspGluAspGlnSerArgGluGl 419
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US-09-320-878-19/C

Sequence 19, Application US/09320878A

Sequence 19, Application US/09320878A

Sequence 19, Application US/09320878A

Sequence 10, 6117659

GENERAL INFORMATION:
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Robert

APPLICANT: TANG Li

TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622001210

CURRENT APPLICANTION NUMBER: US/09/320,878A

CURRENT FILING DATE: 1999-05-28

EARLIER PILING DATE: 1998-05-28

EARLIER FILING DATE: 1998-05-06

EARLIER FILING DATE: 1998-05-28

EARLIER FILING DATE: 1998-05-28
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Conservative:
Mismatches:
Indels:
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US-09-320-878-19
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                                                                                                                              US-09-720-086-8 (1-853) x US-08-923-137-1 (1-35524)
                                                                                                                                                                               Query Match:
                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                 US-08-923-137-1
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APPLICANT: Wilson
                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 35524 base pai
                                                                17568 TCAGTGGCGCTGCGAGGCCTGAACCGCCACGGAAGCTATGCCTGGTATCGCCCCGATCGC 17509
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17508
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NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,700
FILING DATE: 06-SEP-1996
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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CGCGGCTATGATGGGGGATCAGAGCAGGCAGAAAAGCCACCCCCAGCCTCTTGCTGATAGC 17449
                           ArgSerThrArgGlyArgGlnGlyArgAsnHisValAspGluSerProValGluPhePro
                                                                                             AlaValArgThrArgAsnAsnAsnSerValSerSerArgGluArgHisArgProSerPro
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                                                                                                                                                                                                                                                                                                                                                            nucleic acid
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Krishna J.
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Matches:
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à	142	ArgArgArgAlaThrAlaSerAlaGlyThrProTrpProSerPro 161
Ω	17448 (GCGCCGCCGCCTGTG17410
à		ProSerSerTyrLeuThrlleAspLeuThraspAspThr 174
g	17409 (CCCTCTTCTACGGCGCGAGTTTCTTCCTCGGTAGCCAGTAATGGGGACACGAAGGCGGCA 17350
ò		GluaspThrHisGlyThrProGlnSerSerSthrProTyr
q	17349 /	agtgagggccatatctgcaaggaggcagcggcaacaactgttaagttgtgatgcttgggt 17290
ર્જ	189	AlaargLeuAlaGlnAspSerGlnGlnGlyGlyMetGluSer 202
ద	17289 (GGTAGCGTAČĠĊĠŦĠĠĊĂACGTCATGGGATCCGCGĊĠĠĊCATCGCGATACACTCTCCGCA 17230
ò	203	ProGlnValGluAlaAspSerGlyAspGlyAspSerSerGluTyrGln 218
g	17229 (ccasandeadecosadareadarrecrosresededadedecosecesesesereacras 17170
ò	219	
셤	17169	TAGGTGTTTTGCGGCGACGGCGCAAGTACTGCTCCCGCTGCGGTAGTAGCGAGTGCCTC 17110
ઠે	227	Aspleu 228
g	17109	GGTAACCCGGGAGTTGGAATAATAGATGGGTGCAGAGCATAATTTGGCATCAGCAAACTTG 17050
કે	229	ValTrpGlyLyslleLysGlyPheSerTrpTrp
a	17049 (::: CTGGACCGTACTGTCGCCGGGATCTTCGAGTGGTGTTGACGGCAGCTGGAGTTGTAACGG 16990
à	240	
g	16989 (::: GTGCTGACATCCAGGGATCCGTTTGTACCTCAATGGAGGTGGTTGTGGGGCTTTGCAGGTT 16930
8	255	ArgirpValGln-TrpPheGlyAspGlyLysPhese
g	16929 (
8	272	1-SerAlaAspLysLeuValAlaLeuGlyLeu
g	16869 (CTGGCGCCACCTGCTTGATGGGTTCTATATCGGGATCCACTT 16810
à	283	
8	16809	TCATTTTCTCCAGCACGTCCAGCCGCTGGGGCACCATCAATTGCATAGTGG 16750
ò	297	erTyrargLysAlaMetTyrHisAlaLeu
셤	16749 (GATACAGATCCTCACCCTCTCGCTTGATGCCTCTGCGTGGAGGCACGGGCAGCACTTGCT 16690
à	307	GluLysAlaArgValArgAlaGlyLysThrPhePro318
임	16689 (GCAGGGTGACTGGCTTGAGGGTGGGATTCCCATTGTCCAAGGGAATGGACACCG 16630
ò	318	318
용	16629 (CCTCCTCCTTGGGACTGGAGCGGGAGCGCTTGCCATAAGCAAACTCGCCCAGGCGGTCAG 16570
8	319	
q	16569	CCGCCTGCTCCAGAATATCATCATCCCCATACACACTCATAGGACCGCTTAAAAAGCAG 16510
à	332 (etLeuGluTrpAlaHisGlyGlyPheLysProThrGlyIleGluGlyLeuLysProAsnA 352
g	16509	Techegagcecreseceseseradasecaceses recaserereases 16453
ጵ		snThrGlnProValValAsnLysSerLysValArgArgAlaGlySerArgLysLeuG 371
q	16452 (gcactrogeorcca

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16368 396 16308 404 16248 16224	3
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16308 404 16248 16224	ProbysArgLeuLysThrAsn 403
404 16248 420 16224	. ტ
16248 420	TyrAsnAsnGlyLysAspArgGlyAspGluAspGlnSerArgGluGln 419
420	TCCTCGCTGGGACACACAACATCGGA16225
16	tAlaSerAppValAlaAsnAsnLysSerSerLeuGluAspGlyCysLeuSer 437
	GACTGCTCAGTATCTTCTAAGAGCGAGGGGACGGCTGCGCACGGCACGC 16174
Qy 438 C	CysGlyArgLysAsnProValSerPheHisProLeuPheGluGlyGly 453
Db 16173 G	credecedarearoacarcacacacacadikaacatraachtracataridaacarar 16114
Oy 454 -	
Db 16113 T	GGCAATGGCCGCTGCTGCAGTGGCTGCGCGCCTGCGGGACCTGCCACTGGCAC 16054
63	euGlu
Db 16053 C	CTGAAGCCGCGCGTCTGGCTGTTAAGCATAGCTCTTCGCCCCACGCGTTTGGCTCTCC 15994
Qy 465 -	LeuPheTyzMetTyzAspAspAspGlyTyrGlnSerTyrCysThr 479
Db 15993 G	GTAGCAAAGCTCTTGCTGCTTGCTGGGAGTAGCCCGGTGGCGCCCTGGCGATGCGTC 15934
Qy 480 v	ValCysCysGluGlyArgGluLeuLeuLys-SerAsnTh 493
Db 15933 T	rccecciécrerrccaccacacaraccecédécercactactacciórcaraacts 15874
Qy 493 r	rSerCysCysArgCysPheCysValGluCysLeuGluValLeuValGly 509
DP 15873 C	CATCCACAGTAGATGTAGGAGTAGGAGTATAAGTTACGAGCATCGGCCACCACCTGGT 15814
Qy 510 -	ThrGlyThrAlaAlaGluAlaLySLeuGlnGluProTrpSe 523
Db 15813 C	GATCACATCATCGACGGTGGTTCTAGTGCGGATACGGCCCCTTGAGGGCGCCCCCATGGAG 15754
Qy 523 r	CysTyrMetCysLeuProGlnArgCysHisGlyValLeuArgArg538
Db 15753 C	cecegaaGrerecececacrecachegedrererabaacerrreceaecac 15700
- 953 VQ	ArgLysAspTrpAsnValArgLeuGlnAla548
D 15699 C	CTCCGTACATCTTGCTTGGCGCGCGCAGGCCCCAACCGGTGTTATTACTAGGTG 15646
Qy 549 -	
Db 15645 A	
Oy 562 8	SLeuTyrProAlaIleProAlaAlaArgArg 572
Db 15585 A	 CTATGCCCAGGGCCTTGTAGACG
RESULT 10 US-08-760-745-4 ; Sequence 4, Ag; Patent No. 597; GENERAL INPOS; APPLICANT: APPLICANT: APPLICANT: TITLE OF IT	445-4 4, Application US/08760745 5. 5972678 INFORMATION: CANT: Bandman, Olga CANT: Goli, Surya K. CANT: Goli, Surya K. CANT: LUNG GROWTH FACTOR VARIANT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
OPERATING SYSTEM: DO
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STATE: Palo Alto
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ADDRESSEE: INCYTE PHARMACEUTICALS,
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LIBRARY: GenBa
CLONE: 598956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2376 base pairs
                                                                                                                                                                                                                                  GGGTGGAGGAAGAGGCCTCGCGCAGAGAGGAGGAAGCAATTGAATTT----CAAACACAAACA 81
                                                                                                                                                                                                                                                                                                                       GlyArgGlnGlyArgAsnHisValAspGluSerProValGluPheProAlaThrArgSer 145
                         AlaAspSerGlyAspGlyAspSerSerGluTyrGlnAspGlyLysGluPheGlyIleGly 226
                                                                                                                                           AspThrGluAspThrHisGlyThrProGlnSerSerSerThrProTyrAlaArgLeuAla 192
                                                                                                                                                                         GTGCGGCGCGCGGGGGAGACGCCGTGGCCGCGCGGAGCTCGGGGCCGGGGGCCACCATC
                                                                                                                GAGGCGGGGGCCGCGAGGGCCGAGCGGAGCGGAGCGCCACCGCCACCGCCACGCGCAAAC
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SYSTEM: DOS
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                                                                                  -----GlnGlyGlyMetGluSerProGlnValGlu 206
TCGCGATCCAACCGGCAGAAGGAGTACAAATGCGGG
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Matches:
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                                                                                                                  APPLICANT:
APPLICANT:
             APPLICANT: Treadway, Patti J. APPLICANT: Turner, Jan R. APPLICANT: Waldron, Clive TITLE OF INVENTION: Biosynthet: TITLE OF INVENTION: Production NUMBER OF SEQUENCES: 39
                                                                                                                                                                     APPLICANT:
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CORRESPONDENCE ADDRESS
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                                                            Merlo, Donald J.
Treadway, Patti J.
Turner, Jan R.
Waldron, Clive
Waldron, Clive
                                                                                                                                Broughton, Mary C.
Crawford, Kathryn P.
Madduri, Krishnamurthy
                                                                                                                                                                                        Baltz, Richard H.
                                               Biosynthetic Genes For Spinosyn
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29716 CGCACCGCCGCGAACGACTTGCACCGCCCATCCGGCGCGAGACCCCCGTTGGCGGGAGAA 29657
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                                                                STATE:

COUNTRY: USA

ZIP: 46268

ZIP: 46268

COMPUTER 19099 disk

COMPUTER: Floppy disk

COMPUTER: IBM PC compatible

CORRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/036,987A

TIING DATE: 09-MAR-1998

TILING DATE: 09-MAR-1998
ADDRESSEE: Dow AgroSciences LLC Patent Department STREET: 9330 Zionsville Road CITY: Indianapolis STATE: Indiana
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Matches:
Conservative:
Mismatches:
Indels:
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ATTORNEY AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 20,608
REFERENCE/DOCKET NUMBER: 50,608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317)337-4816
TELEFAX: (317)337-4847
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 80161 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
NOLECULE TYPE: DNA (genomic)
US-09-036-987A-1
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Best Local Similarity:
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2	00000	6262
රි රි	Oy 148 gArgAlaThrAlaSerAlaGly	155
3 8	156ThrProTrpProSerProPr	acercenn 2523
qq	29236 CTCCGACACGC	CCAGGACGATCGGA 29177
ò	169	ThrProGlnSerSe 184
a	Db 29176 GTCCGGAACGACACCCCATCCAGGTCCCCACGGATCCCCCGGAACTTCGGAGATCGC	ACTTCGGAGATCGC 29117
ò	184	MetGluSer 202
QQ	Db 29116 GTCCACACCGCGCCAGCCAGTTGCCACAGGTCCTCCGGCGAGGAGACCTGACC	GAGGAGCCTGACC 29063
ò	Qy 203ProGlnValGluAlaAspSerGlyAspGlyAspSerSerGluTyrGlnAsp	GluTyrGlnAsp 219
d	29062 GGGATAA	TCCGCGGAGAACCG 29003
ò	Oy 220GlyLysGluPheGlylleGlyAsp-LeuValTrpGlyLyslleL	TrpGlyLyslleL 234
QΩ	Db 29002 ATCCCTGCCGCGCGCGGAGGCGTTCGTTCTTGAGCGATGCTCGCAGTGCCTCGACAA	AGTGCCTCGACAAC 28943
ò	234 ysGlyPheSerTrpTrpProAlaMetValValSer	rSerLysArgGlnA 254
q	28942 TTCTTCGTAACTCG	rdercaccercarcaccaderced 28904
\$ 5	254 laMetSerGlyMetArgTrpValGlnTrpPheGlyAep 28403 [Ser 273
3 6		י פיטורפיטי
2 6	CY 2/4 ALGASPLYSLEUVALALEUGLYLEURDSSETCHINISPREAGNIEUALBINE D 28843 TCGATCGAGGTCGCGGCCGCATCGTCCGAGGAGATACCGGAGTCGACCGGGGTGT	
ò	Qy 292PheAsnLysLeuValserTyrArgLysA	ysAla 301
å	28789 CCGCCAAGTGCGAGCAGCGGACTCACCAAGCCTGCCTCG	 -CGCAAGGCCGGGAACGGG 28733
δ	Qy 302MetTyrHisAlaLeuGluLysAlaArgValArgAlaGlyLysThrPheProSer	ysThrPheProSer 319
qq	28732	TGCCTGCTCTGCG 28673
ò	320 SerProGlyAspSerLeuGluAspGlnLeuLysProMetL	euGluTrpAlaHisGlyGly 339
ор	28672	CGCAGCTCCGCA 28640
ò	340 PheLysProThrGlyIleGluGlyLeuLy	enThrGlnProVal 356
qq	Db 28639 GCCAGTTCCGCAGGCGTGGGATGGCTGAGATAATTGTCGATGGCAACTGGAGGCCGGTA	ACTGGAGGCCGGTA 28580
ò	357 ValAsnLysSerLysValArg	erArgLysTyrGlu 376
qq	28579 GCTCGATTGAGCCGAACG	CGAATCCGCTGTCC 28523
ò	Oy 377 AsnLysThrArgArgArgThrAlaAspAspSerAlaThrSerAspTyrCysProAlaPro	YrCysProAlaPro 396
đ	28522 TTGAAGGCT	GGTGTCCCAGCACC 28472
δ	397	yrAsnAsnGly 407
Q	28471 AGAGCGGTTTC	rcggccrcdgrgcc 28412
ò	Qy 408LysAspArgGlyAspGluAspGluSerArgGluGlnMetA	etAlaSerAspVal 424
q	Db 28411 GCGGACAATCGCTGCCGCCATTCCAACGACGCGTCGGCAAGGACTCCCGCCTCGGGCTGG	cceccree 28352
ò	Qy 425 AlaAsnAsnLysSerSerLeuGluAspGlyCysLeuSerCysGlyArgLysAsnPro	lyArgLysAsnPro 443

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DB:
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APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Kathryn p
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Turner, Jan R
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Sp
FILE REFERENCE: 50489 DIV1
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT APPLICATION NUMBER: US/09/370,700
EARLIER APPLICATION NUMBER: US/09/36987
EARLIER APPLICATION NUMBER: US/09/36987
EARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
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                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09370700 Patent No. 6274350
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                                                                                    GGCATCCGACAACCGCTCCAGCAACAACAGTCCGGCACCCTCACCCCATCCAGTGCCATC
                                                                                                           AlaIleArgThrPro----
                                                                                                                                                             SerIleLeuValAsnGlyAlaCysSerAspGlnSerSerAspSerProProIleLeuGlu
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ThrGlnAspLeuThrGlyAspGlyAspGlyGluAspGlyAspGlySerAspThrProVal
                                   CGCACCCGCCGCGAACGACTTGCACCGCCCATCCGGCGCGAGACCCCCGTTGGCGGGAGAA
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Matches:
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28639 GCCAGTTCCGCAGGCGTGGGATGGCTGAAGATAATTGTCGATGGCAACTGGAGGCCGGTA 28580
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                                                          PheLysProThrGlyIleGluGlyLeuLys-----ProAsnAsnThrGlnProVal 356
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US-09-720-086-8 (1-853) x US-09-491-772-1 (1-8580)	Oy 85 ProValMetProLysLeuPheArgGluThrArgThrArgSerGluSerProAlavalArg 104	105 ThrArgAshAshSerValSerSerArgGluArgHi8Arg		12 1 24 1 1 1 24 1 1 1 1 1 1 1 1 1 1 1 1	143 rArgSerLeuArgArgArgAlaThrAlaSerAlaGlyThrProTrpProSerProProSe	Qy 163 rSerTyrLeuThr-IleAspLeuThrAspAspThrGluAspThrHisG 179	Qy 179 ly-ThrProGlnSerSerThrProTyrAlaArgLeuAlaGlnAspSerGlnGlnGly 198	Gly	211 AspdlyAspSerSerGluTyrGlnAspGlyLysGluPheGlyIleGlyAspLeuValTrp ::::::::::::::::::::::::::::::::::::	231 GlyLyslleLysGlyPheSerTrpTrpProAlaMetValValSerTrpLysAlaThrSer 6229	251 LysargGlnalametSerGlymetArgTrpValGlnTrpPheGlyAspClyLysPheSer	0y 271 Glu	for dy 272 ValSerAlaAspLysLeuValAla 279	Oy 280LeuGly	285 GlnHisPheAsnLeuAlaThrPheAsnLysLeuValSerTyrArgLysAlaMet AlaThrPheAsnLysLeuValSerTyrArgLysAlaMet AlaThrPheAsnLysLeuValSerTyrArgLysAlaMet	303 TyrHisAlaLeuGluLysAlaArgValArgAlaGlyLysThrPheProSerSerProGly	Qy 323 AspSerLeuGluAapGlnLeuLysProMetLeuGluTrpAlaHisGlyGlyPheLysPro 342	
7 () () () () () () () () () (UY 357 VALABILIYBSELIYBVAIATGALGALGALGALGALGALGALGALGALGALGALGALGALG	<pre>Qy 377 AsnLysThrArgArgArgTrAlaAspAspSerAlaThrSerAspTyrCysProAlaPro 396</pre>	Qy 397 Ly8	Oy 408LysAspargGlyAspGluAspGlnSerArgGluGlnMetAlaSerAspVal 424	425 AlaAsnAsnLysSerSerLeuGluAspGlyCysLeuSerCysGlyArgLy8AsnPro 28351 GCATCGACGAGGAGTTCCTTGACCTCGGCCAGTTCGTTCAGCAGCGGCGCCGC	444 ValSerPheHisProLeuPheGluGlyGlyLeuCysGlnThrCysArgAspArgPheLeu	Oy 464 GluLeuPheTyrMetTyrAspAspAspGlyTyrGlnSerTyrCysThrValCysCysGlu 483 ::: Db 28285	Oy 484 GlyArgGluLeuLeuLeuCy8SerAsmThrSerCy8Cy8ArgCy8PheCysValGluCys 503	Oy 504 LeuGluValLeuValGlyThrGlyThrAlaAlaGluAlaLysLeuGlnGluProTrpSer 523	Oy 524 CysTyrMetCysLeuProGlnArgCysHisGly 534 Db 28150 CCTGTTTCTCCGGAGGCCATGCCCTCGCGGCCCACGGC 28112	RESULT 13 US-09-491-772-1 ; Sequence 1, Application US/09491772 ; Patent No. 6329172.	GENEKAL INFORMATION: APPLICANT: Rhee, Joon Shick APPLICANT: Pan, Jae Gu APPLICANT: Ahn, Jung Hoon	Science and Technology(KAIST) Gene Cluster in Pseudomonas fluorescens retion		R OF SEQ ID NOS: ARE: KOPATIN 1 NO 1	7 X X	Alignment Scores: 0.535 Length: 8580 Pred. No.: 126.00 Matches: 104 Percent Similarity: 34.84\$ Conservative: 42	: 24.82% Mismatches: 1

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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                           Alignment Scores:
                  US-09-720-086-8 (1-853) x US-09-179-558-54 (1-2874)
                                                                                                                                                                                                              US-09-179-558-54
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ent No. 6180612
ERAL INFORMATION:
APPLICANT: Hockensi
APPLICANT: Muthusw
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 9426-005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
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APPLICATION NUMBER: U.S.
FILING DATE: 31-OCT-1997
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: U.S.
FILING DATE: 15-APR-1998
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TITLE OF INVENTION: METHODS AF
TITLE OF INVENTION: TARGETING
TITLE OF INVENTION: AMINOGLYCO
                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                        No.:
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                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 8699741
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                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                          281 ---GlyLeuPheSerGlnHisPheAsnLeuAlaThrPheAsnLysLeuValSerTyrArg
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360 SerLysValArgArgAlaGlySer----
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1777 GCCGTCAGGCCGACCTTCTTCCCTCAGTTCCATGCCTTTGGACTTCGCTACTGTGGCGCC 1836
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                                           685 LysGluGlyAspAspArgProPhePheTrpMetPheGluAsnValValAlaMetLysVal 704
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| Patent No. 6048710|
| GENERAL INFORMATION|
| APPLICANT GURX, Wilhelmus J.
| TITLE OF INVENTION|
| TITLE OF INVENTION|
| TITLE OF INVENTION|
| TOWNERS OF SEQUENCES|
| OWNERS OF SEQUENCES|
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| ADDRESSEE Genencor International
| STREET 925 Page Mill Road
| CITY: Palo Alto
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COUNTRY: CA
COUNTRY: CA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,853
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/911,853
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/91,052
FILING APPLICATION NUMBER: 08/699,092
FILING APPLICATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: 33,888
REFERENCE/DOCKET NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GG361-2
TELLEPHONE: 650-846-7620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 17612 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13146 CCCCTGGGGCAACCAGTACCTGTACCTGTCGCCGGGCACCCCGCGGCAAGATCGACCTGTA 13205
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224 GlyfleGlyAspLeuValTrp-----GlyLysfleLysGlyPheSerTrpTrpProAla 241
                                                                                                                                                                                                                                                                                              165 TyrLeuThrIleAspLeuThrAspAspThrGluAspThrHisGlyThrProGlnSerSer 184
                                                                                                                                                                                                                                                                                                                                                              152 AlaSerAlaGlyThrPro-----Trp------ProSerProProSerSer 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 ArgGluThrArgThrArgSerGluSerProAlaValArgThrArgAsnAsnAsnSerVal 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ArgGluValSerSerLeu-------LeuSerTyrThrGlnAspLeuThr 71
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                                                                                                                               -----GCTCGAGCTGGAGATCGAGGTCGACGAGCAGAGTGTCGGGCTGCCCGCCGC--- 13628
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                                                               -----CCGTGGCGAGCAGGACAAAGCCGCGGCCAAGGCGCCACAGCTGCT 13673
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eProAlaAlaArg	TCG 1	nAlaPhePheThrSerAspThrGlyLeuGluTyrGluAlaProLysLeuTyrProAlaIl 5	steurroginargcyshisclyvalteuargargarguysaspirpasnvalargteugt 5 :: :: CCGCGACACCCAGCTGGAGTTCACCCGCAGCCG		val-GlyInrelyInrelaalaguw4.aalysLedGlnGlnGlnGrnGrgerysTyrmecCy >		LeuLeuCysSerAsnThrSerCysCysArgCysPheCysValGluCysLeuGluValLeu 5		4	1	heGluGlyGlyLeuCysGlnThrCysArgAspArgPheLeuGluLeuPheTyr 4	AGCGCGGCTTCACCCTGCTGGAAGTGCTGATCGCCATCGCCATCTTCGCCCTGCTGGCCA 1	4.	AGATCGAAGACCATGCCCTGGTGACCCTGAGTGGCTTCGTCGGGGGTCGAGCCATGAGGC- 1	r 4	⊢ +	euLysThrAsnCysTyrAsnAsnGlyLysAspArgGlyAspGluAsp 4	TG 1	TyrGluAsnLysThrArgArgArgThrAlaAspAspSerAlaThrSerAspTyrCysPro 3	CCGCGAGCAGGGGGGGAGAGCTACGCCGGGCGGCGCGCTGGCTG	w	:::: GGCGGACAACCGCCTGCAGGAGGTGCCGGCGAGGG 1	w	ThrPheProSerSerProGlyAspSerLeuGluAspGlnLeuLysProMetLeuGluTrp 3	-	GlyLys 3		LeuValAlaLeuGlyLeuPheSerGlnHisPheAsnLeuAlaThrPheAsnLysLeu 2	ົດ	SerGluValSerAlaAspLys 2	CGGCGCGCGGTGCTGACGCCAGCGACGGCTT	PerGlyMetArgTrpValGlnTrpPheGlyAspGlyLysPhe 2
4549	4489	67	4472	;	14439	1 393	07	14345	187	14306	67	4255	49	.4195	129	.4136	114	4091	94	,A	174	4	4	3546	3907	115	13862	295	13835	276	13775	269

Qy 578 uSerLeuPheAspGlylleAlaThrGly 587

Db 14550 GCGCTTACTGGACGGTGCTGGACCAGGC 14577

Search completed: November 25, 2002, 03:06:35 Job time : 473.863 secs

Mon Nov 25 08:18:41 2002

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RESULT 1
US-09-276-531-47
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Patent No. 6183968

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Olga
APPLICANT: Yue, Henry
CANT: Reddy, Roopa
APPLICANT: Reddy, Roopa
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
NUMBER OF SEQUENCES: 134
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Word Perfect 6.1 for Windows/MS-DOS 6...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,531
FILING DATE: Herewith
CLASSIFICATION DATA:
APPLICATION UNDATA:
APPLICATION UNDATA:
PRIOR APPLICATION DATA:
APPLICATION MARCH: 60/079,677
FILING DATE: March 27, 1999
CLASSIFICATION:
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ADDRESSEE: INCYTE PH
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CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ATTORNEY/AGENT INFORMATION
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US-09-105-537-30
US-08-125-468-1
US-08-474-933-1
US-08-307-621-1
US-09-307-621-1
US-09-804-227-216A-7
US-09-147-236-1
US-09-147-236-1
US-09-147-236-1
US-09-103-840A-1
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RESULT 2
US-08-913-832A-1
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TESTTUT02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008
TELECOMMUNICATION INFORMATION:
TELECHHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2077 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                           AspTyrPheAlaCysGlu 853
                                                                                                                       LysLeuLeuGlyArgSerTrpSerValProValI1eArgHisLeuPheAlaProLeuLys 847
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Conservative:
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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODB=LOCAL -QUTPMT=pto -NORM=sxt -HBADSIZE=500 -MINLEN=0 -NAXLEN=200000000
-USER=US09720086 @CGN 1 1 108 @runat 18112002 092957 29457 -NCPU=6 -ICPU=3
-NO XLPXY -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched
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Ygapop 10.0 , 1
Fgapop 6.0 , 1
Delop 6.0 , 1
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4935
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-804-227C-1
US-08-458-568A-11
US-07-853-913-3
US-08-629-939-1
US-08-759-873-1
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Patent No. 6
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ALIGNMENTS

Henry Preeti Olga

Jennifer L.

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
NUMBER OF SEQUENCES: 134
                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                            CITY: PALO ALTO
STATE: CALIFORNIA
                                           APPLICATION NUMBER: 60/079, FILING DATE: March 27, 1998
                                                                                                                                                APPLICATION NUMBER: UPFILING DATE: Herewith
                          CLASSIFICATION:
                                                                                                                      CLASSIFICATION:
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727 ThrGlyArgLeuPhePheGluPheTyrArgLeuLeuHisAspAlaArgProLysGluGly 746
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Matches:
Conservative:
Mismatches:
Indels:
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NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42.918
REPERENCE/DOCKET NUMBER: PA-0008 US
TELECOMMUNICATION INFORMATION:
TELEPRONE: (650) 845-0555
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2077 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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748.00
81.95%
73.66%
15.16%
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Best Local Similarity:
Query Match:
DB:
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US-09-105-537-1/c
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10619 CGGAGATCACCGACCGGGGCCGTTCA-----CCGCGGCGACGCAGGCGT 10569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 nileGluSerMetLys-----MetGluGlySerArgGlyArgLeuArgGlyGlyLeu-- 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 AspLeuGluLysArgSerGluProGlnProGluGluGlySerProAlaGlyGlyGlnLys 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 Pro-----ProValGluSerGlyAspThrProLysAspProAlaValIleSerLys 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 SerProSerMetAlaGlnABpSerGlyAlaSerGluLeuLeu------ProAsnGly 91
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Patent No. 6265202
GRNRRAL INFORMATION:
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Abo, Y.
APPLICANT: Abo, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REPERENCE: 600.438081
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PERESEQ for Windows Version 3.0
SSP IND NO.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Streptomyces venezuelae
JS-09-105-537-1
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32.84%
22.39%
3.70%
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Best Local Similarity:
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Best Local Similarity:
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                                                                           Score:
US-09-720-086-7 (1-912) x US-08-804-227C-1 (1-43280)
                                    Query Match:
                                                                                                    Alignment Scores:
                                                                                                                             US-08-804-227C-1
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SEQUENCE CHARACTERISTICS:
LENGTH: 43280 base
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
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APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                                                                                                                                                                                                                                  FEATURE:
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CURRENT APPLICATION DATA:
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TOPOLOGY: lir
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                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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38 ArgGlnGluProSerThrThrAlaArgLysValGlyArgProGlyArgLysArgLysHis	92 AspLeuGluLysArgSerGluProGlnProGluGlySerProAlaGlyGlnLys	### ##################################		GlyTrpGluse rcGTGGGCCAT	185MetProArgLeuThrPheGlnAlaGlyAspProTyrTyrIleSerL	200 ysargLysargaspGluTrpLeualaargTrpLysargG	213 lualaGluLysLysBlatysValIleAlaGlyMetAsnAlaValGluGluAsnGlnGlyP	233 roGlyGluserGlnLysValGluGlu	243 erproproalavalginginprothrapproalaserprothrvalalathrThrpro-	63GluprovalGlySeraspAlaGlyAspLysAsnAlaThr	276	20		289 lyPheGlyIleGlyGluLeuValTrpGlyLySLeuArgGlyPheSerTrpTrpProGlyA
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APPLICANT: Schaffer, Priscilla A. APPLICANT: Schaffer, Priscilla A. APPLICANT: Yeh, Lily TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus TITLE OF INVENTION: Infections NUMBER OF SEQUENCES: 15 CORRESPONDENCE ADDRESS: ADDRESS: Moodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris STREET: One Liberty Place, 46th floor CITY: Philadelphia
                                                                                                                                                                                                                                                          37341 CGGAGGGGGGGAGCAGCGCCCGGCCTCGATGGGGTCGCCGGGTGCCGGTG---- 37286
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309 rgileValSerTrpTrp------MetThrGlyArgSerArgAlaAlaGluGlyThrA 326
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-458-568A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3439
TELEPAX: (215) 568-3100
TELEPAX: (215) 568-31100
TELEPAX: (215) 568-31100
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,146
FILING DATE: 05-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: DFCI-0029
                                                                                                                                                                                                                                                                                                                                                                6189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6021 TCGTCCGGACGGCCTCCTCTACCATGGAGGCCAGCAGAGCCAGCTGTCGCGGCGAGACGG 6080
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                                                                        6290 CGCTGCTTGTTCTCCGACGCCATCGCCGATGCGGGGGGGTCCTCCGGGGATACGGCTGCG 6349
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                              107
138 ThrProLysGluGlyArg-GlyAlaProAlaGluAla-----GlyLysGluGlnLysGl 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         961 CGTCGTCGGCTCGAAAGGCGGGGGTCCGGGGCGGCGAGGCCGCGGGGTCGGGCGTCGGGA 6020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 -----LysAspGlyGluGluGluGluGluFroArgGlyLysGluGluArg 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 Gln---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 ProSerSerGlyProGlyAspThrSerSerSerAlaAlaGluArgGluGluAspArg---
                                                                                                                                                                                                                                                                             -----AlaGlyGlyGlnLysGlyGlyAlaProAlaGluGlyGluGlyAla------
                                                                                                                                                                                                                                                                                                                                                                CGCCCT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspProAlaVallleSerLysSerProSerMetAlaGlnAspSerGlyAlaSerGluLeu 87
                                                                                                                                                                                                                  CGTCGCGGTCTGGGCTCGGG-GTGGGCGGCGGCCCGTCGGTGGGGCCCCGGGAGCCGGGG-6289
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                                                                                                                                          --AlaGluThrLeuProGluAlaSerArgAlaValGluAsnGlyCysCys 137
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Db 4470 GYGGGANAAAGACAGGGACGGCCCCCCCCCCCCCCCCCCC
6470 6516 6516 6516 6629 6656 6629 6656 6629 66807 68807 300 300 310 310 310 310 310 310 310 310
6470 194 6516 208 6556 216 6629 6656 2707 6707 6807 300 68822 340 380
6470 194 6516 208 6556 216 6656 256 6656 6707 280 6807 300 6882 340 6882
175 6470 194 6516 208 6569 216 6629 236 6656 256 6707 280 6767 280 6807 300 6882 340
6470 194 6516 208 6556 216 66629 236 66656 6767 280 6882 340
6470 194 6516 208 6556 216 6629 236 6656 256 6707 280 6807 300 6822
175 6470 194 6516 208 6569 216 6629 236 6629 256 2707 262 262 300 6807 320
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175 6470 194 6516 208 6569 216 6629 236 6656 6707 262 280
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6470 194 6516 208 6569 216 6629 236 6656 676707
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6470 6516 208 6569 216 236 236
6470 194 6516 208 6569 216 6656
1/5 6470 194 6516 208 6569 216
1/5 6470 194 6516 208 6569 216
1/5 YITDJUSETSETLEUATGUTNATGYTOMEG PYTOMEG THAI 6470 GTGGGAAAAAGGACAGGGACGGCCGATCCCCTCCCGCGCTTCGTC 194 pProTyrTyr1leSerLysArgLysArgAspGluTr 194 pProTyrTyr1leSerLysArgLysArgAspGlu
1/5 YITDGIUSETSETLEUATGGINATGFTOMETPOATGGEUTNTPHEGINAIGG
1/5 Y!!pG1U 6470 GTGGGAA
1/5 YITGGIUSETSETLEUATGGIDATGFTOMEEFTOATGFEUTDTPDEGIDATGGEGGTTCGTC
1/5 YTTpGLUSerSerLeuArgGLDArgProMetProArgLeuTDrPneGLDAL8G1
10 (Mary 1:0) (1) (1) (1) (1) (1) (1) (1) (1) (1) (1
Db 6410 CACGGACCCCGACGACCCCCCCCGTCGACGCGGAACTAGCGCGGACCGGTCGATGCTTGG
Db 6350 ACGCCGACGTAGCACGTAGGTCACCTACGGACTCTCGATGGGGGGAGGGGCGAGAC

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7100 CGGCCGGGACCGCCCCAAGGGGGCGGGCCGCCGCCGGTAAAAGAAGTGAGAACGCGAAAGCG 7159
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                                                                          1160 TTCGCACTTCGTCCCAATATATATATATAGGGCGAAGTGCGAGCAC 7209
                                                477 ------GluArgLeuValTyrGluValArgGlnLysCysArgAsn 489
                                                                                                                                                             US-07-83-913-3
Sequence 3, Application US/07853913
Sequence 3, Application US/07853913
Sequence 3, Application US/07853913
Sequence 3, Application US/07853913
Sequence 3, Application: Application: APPLICANT: Lendahl, Urban
TITLE OF INVENTION: Nestin Expression As An Indicator of TITLE OF INVENTION: Nestin Expression As An Indicator of NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: TWO Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.

ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/660,412
FILING DATE: 19920319
CLASSIFICATION NATA:
APPLICATION NUMBER: US 07/660,412
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,803
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,762
FILING DATE: 02-UNU-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/180,548
ATTORNEY/AGENT INFORMATION:
NAME: Grandan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4641AAAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-661-6240
TELEFAX: 617-861-6240
TELEFAX: 617-861-6240
TELEFAX: 617-861-6240
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Matches:
Conservative:
Mismatches:
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MOLECULE TYPE: DNA (genomic)

US-07-853-913-3
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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3705	3679CGATCCTGGAAGATGCCCCTGGGCTC	qq
290	271 AspLysAsnAlaThrLysAlaGlyAspAspGluProGluTyrGluAspGlyArgGlyPhe	ò
3678		QQ
270	251 ThrAspProAlaSerProThrValAlaThrThrProGluProValGlySerAspAlaGly	ò
3663	Ft	qq
250	231 GlnGlyProGlyGluSerGlnLyBValGluGluAlaSerProProAlaValGlnGlnPro	ò
3603	3544 GGAGCAGAGGAGGCGTTCCCTGCTGAGACCCTGGGCCACACTGGAAGTGATGCCCCTTCA	qq
230	213 GlublaGluLysLysAlaLysVallleAlaGlyMetAsnAlaValGluGluAsn	ò
3543	3484 AGAGACCTTGGGAGCCTCCCCAGGGAGGAGGAGGAGGACTCAGAGGCTGAGGCCCCCCAGG	qq
212	193 GlyAspProTyrTyrIleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArg	ò
3483		qQ
192	GlnArgProM	ò
3444	3385 TTGGAGGCAAAGAGGGTTCAGGGCTTGGAAGGGCCTAGAAAGGACCTAGAGGAGCAGGT	q
172	158 IleGluSerMetLyBMetGluGlySerArgGlyArgLeuArg	ò
33	3325 GGGGACCCCATCTGACCAGGGAAGAGGTGATGGAACCACCCCTGGAAGAGAGAG	Ω
157	144 GlyAlaProAlaGluAlaGlyLysGluGlnLysGluThrAsn	ò
3324	3265 GCCATGGGTGAGTCTGCTGCGGAGCTGAGCCTGGGGCAGGGGTGGGAGGCTG	qq
143	129SerArgAlaValGluAsnGlyCysCysThrProLysGluGlyArg	ò
3264	3205 GATGATGTGGCCCCCAGGGGGTGACCAAGCCTCCCCAGAGGTCATGTTGGGGTCAGAGCCT	q
128	128	ò
3204	3145 GGGACCCCAGGCCTCCAGGCTCCCCAGGGCTGCCAGAGGCGATAGAGCCCCTGGTGGAA	d D
128	-	ò
3144	 GGGAGGGGCTGAGGCCTCCAGGACCCTGAAGGGCAATCA	q
120	104 GlySerProAlaGlyGlyGlyGlyGlyGlyAlaProAlaGluGlyGluGly	ò
3084	SAGGCCTGC	g
103	99	ò
3024	2965 ACTGGGAAGGAGGAGGTGGTAGAGCAGGAGAGCTGAATGCCACAGAGGAGGTCTGGTTC	යු
98	83GlyAlaSerGluLeuLeuProAsnGlyAspLeuGluLysArgSerGlu	ò
2964	2905 ATGGCTGGAGTGGAAAATAAGGATGAGGCAGAGCTGAATCTAAGGGAGCAGGATGGCTTC	Dp
82	82	ò
7	2845 CAGAGGTGGGAAGATACGGTGGAGGACCAAGAACTGGCTCAGGAAGCCCTCCTGGG	OC.
82	ValileSerLygSerProSerMetAlaGlnAgpSe	ò
2	2797 AGGTCTCTGGAGGAGGAGGACAGGAGCTGCCGCAGTCTGCAGATGTG	엄
65	46 ArgLysValGlyArgProGlyArgLysArgLysHisProProValGluserGlyAspThr	ò
2796	2749 CTGGAAGAGGAAGAGAACCTGGGAAAGGGAGAGTACCAAGAGTCACTG	QO
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                                                                                                                                                                                                                                                                                                       RESULT 6
                                                                                                                                                                                                                                           Sequence 1, Application US/08629939
Patent No. 5645995
GENERAL INFORMATION:
                                                                                                                   TITLE OF INVENTAL.

TITLE OF SEQUENCES: 14

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZI

CTREET: 2100 Pennsylvania Av
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3792
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                   APPLICANT: Kieback, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                    4176
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                                                                                       ZIP:
                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValSerTrpTrpMetThrGlyArqSerArgAlaAlaGluGlyThrArgTrpValMetTrp 330
                                                                                                                                                                                                                                                                                                                                                                                                                       HisProLeuPheValGly-----GlyMetCysGlnAsn------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGGCCTCCAGGAGGAAGGGGAGGAGAGCAGAGAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProValCysHisAspSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysGluIleIleAspGluArgThrArgGluArgLeuValTyrGluValArgGlnLysCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrAlaProProProProAlaLysLysProArgLysSerThrAlaGluLysProLysVal
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                                                                                                                                                                                                                                                                                                                                  TGCTAC
                                                                                                                                                                                                                                                                                                                                                               CysPhe 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgAsnIleGluAspIleCysIleSerCysGlySerLeuAsnValThr-----LeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuGlyGlyPhe-----GlnProSerGlyProLysGlyLeuGluProProGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspGluSerAspThrAlaLysAlaValGluValGlnAsnLysProMetIleGluTrpAla 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLysAlaIleTyr 370
                                                                            20037
                                                                                                               Washington,
: D.C.
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RISK OF
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 IleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTrpGlu
                                                                                                                                                                                                                                                                                      138 ThrProLysGluGlyArgGlyAlaProAlaGluAlaGlyLysGluGlnLysGluThrAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 TCC-----CTCCTCCCTGGAGACGGGGAGAAAAAGGGGAGTCCAGTCGTC
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 SerGlyAlaSerGluLeuLeuPro---AsnGlyAspLeuGluLysArgSer------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: KIT, Gordon
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/
FILING DATE: 12-APRIL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 AACACCCACTITCTCCTCCCTCTGCCCCTATATTCCCCGAAACCCCCTCCTCCTTCCCTTT
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                                                                                                                                                                                                                                                                                                                                            AlaAlaGluThrLeuProGluAlaSerArgAlaValGlu-----AsnGlyCysCys
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                     AlaLysValIleAlaGlyMetAsnAlaValGluGluAsnGlnGlyProGlyGluSerGln
                                                                 ---AGTCCCCCAGAAAAGGACAGCGGACTG
                                                                                           IleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLysLys
                                                                                                                                                        SerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTyrTyr 197
                                                                                                                                                                                                                                                        TTCCCTCGGCCCTGCCAGGGACAGGACCCCTCCGACGAAAAGACGCAGGACCAGCAGTCG
                                                                                                                                                                                                                                                                                                                      ACCTCGGACACCTTGCCTGAAGTTTCG---GCCATACCTATCTCCCTGGACGGGCTACTC
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à i	238	LysvalGluAlaSerProProAlavalGlnGln 249
Ω	260	9
ò	250	ProThrAspProAlaSerProThrValAlaThrThrProGluProValGlySerAspAla 269
g	608	CCCGAACTTCCCGAAGATCCACCGGCTGCCCCGCCACCCAGCGGGTGTTGTCCCCGCTC 667
ò	270	GlyAspLysAsnAlaThrLysAlaGlyAspAspGluProGluTyrGluAspGlyArgGly 289
qq	668	ATGAGCCGGTCCGGGTGCAAGGTTGGAGACGCTCC
ò	290	PheGly11eGlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrpTrpPro 307
QQ	704	GGGACGCCATGCCCCCTGCCCCCGGGGCCTGTCACCA 748
ò	308	GlyArgileValSerTrpTrpMetThrGlyArgSerArgAlaAlaGluGlyThrArgTrp 327
qq	749	GCCCGG754
ò	328	ValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLeu 347
Db	755	CAGCTGCTGCCCGGCC 772
ò	348	SerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLys 367
q	773	TCTGAGAGCCCTCACTGGTCCGGGGCCCCAGTGAAGCCGTCTCCGCAGGCC 823
ò	368	AlaileTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProValCys 387
QQ	824	GCTGCGGTGGAGGTTGAGGAG
ઠે	388	HisAspSerAspGluSerAspThrAlaLysAlaValGluValGlnAsnLysProMetIle 407
QQ	845	GAGGATGGCTCTGAGTCCGAGGAGTCCGGTTCTGAAGGGCAAACCTCGG 901
ò	408	GluTrpAlaLeuGlyGlyPheGlnProSerGly
QQ	902	GCTCTGGGTGGCGCGGCTGGAGGAGCCGCGCTGTCCCGCGGGGGCG 955
ò	422	
qq	956	GCAGCAGGAGGCGTCGCCCTGGTCCCCAAGGAAGATTCCCGCTTCTCAGCGCCCAGGGTC 1015
ò	436	TyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProProProAlaLys 455
οp	1016	GCCCTGGTGGAGCAGGACGCGCCGATGGCGCCCCGGGGGC 1054
ò	456	LysProArgLysSerThrAlaGluLys
QQ	1055	recederageccaccadedargarancarecaegracerarecracerecareareae 1114
ò	469	GluIle1leAspGluArgThrArgGluArgLeuValTyrGluValArgGlnLysCysA 488
q	1115	GCCTTATTGGCAGCCCGCACTCGGCAGCTGCTGGAAGACGAAAGTTACGACGGCGGGGCC 1174
ò	488	rgAsnlleGluAspileCyslleSerCysGlySerLeuAsnValThrLeuGluHis-Pro 507
QQ	1175	descrecenses de la consecue de la co
ò	508	LeuPheValGlyGlyMetCysGlnAsnCysLysAsnCysPheLeuGluCysAlaTyrGln 527
Ср	1232	GTCGCTGTAGGCGACTTCCCCGACTGCGCGTACCCG 1267
ò	528	TyrAsp
qq	1268	CCCGACGCCGAGCCCAAGGACGCGTACCCTCTATAGCGACTTCCAGCCGCCCGC
ò	540	CysCysGlyGlyArgGluVal 546
qq	1328	CTAAAGATAAAGGAGGAGGAAGGCGCGGAGGCCTCCGCGCGCTCCCGCGGTTCCTAC 1387

ŝ	AsncyscysArgcysPhecysValGlucysValAspLeuLeu	266
qq	1388 CTTGTGGCCGGTGCCAAC	1405
ò	567 ValGlyProGlyAlaAlaGlnAlaAlaIleLy8GluAspPro-TrpAsnCysTyrMetCy 58	586
qq	1406	1433
ò	TyrGlyLeuLeuArgArgArgGluAspTrpProSerArgLeuGl	909
q	1434 -GGCCACCGCCCCGCTGCCGCCGCGACCCCCATCCA 14	1472
δ	606 nMetPhePheAlaAsnAsnHisAspGlnGluPheAspProProLysVa 62	622
qq	1473GACCCGGGGAAGCGGCGGTGACGGCC 14	1498
ò	622 lTyrProProValProAlaGluLysArgLysProlleArg 635	
qq	1499 GCACCCGCCAGTCTCGTCTGCGTCTCCGG 1538	
RESULT US-08-	SULT 7 -08-759-873-1	
 D un (equence 1, Application US/U8/398/3 Satent NO. 5683885 Cement inspondence.	
	APPLICANT: Kieback, Dirk G.	
	TITLE OF INVENTION: METHODS FOR DIAGNOSING AN INCREASED RISK TITLE OF INVENTION: OF BREAST OR OVARIAN CANCER	
	ION, ZINN, MACPEAK	
	2100 Pennsylvania Avenue, N.W., Su	
	0 17	
٠	COUNTRY: U.S.A.	
	COMPUTER READABLE FORM:	
٠	MEDIUM TYPE: Floppy disk COMPITTER: TRM PC compatible	
٠	SOFTWARE: Patentin Release #1.0, Version #1.25	
.	APPLICATION NUMBER: US/08/759,873	
٠	FILING DATE: 12-APRIL-1996 CLASSIFICATION: 435	
	ATTORNEY/AGENT INFORMATION:	
	NAME: KIT, Gordon REGISTRATION NIMBER: 30 764	
	REFERENCE/DOCKET NUMBER: A-6612	
	TELECOMMUNICATION INFORMATION:	
	TELEFAUNE: (202) 293-7860	
٠,	INFORMATION FOR SEQ ID NO: 1:	
	SEQUENCE CHARACIERISTICS: LENGTH: 3014 base pairs	
٠.	TYPE: nucleic acid	
	STRANDEDNESS: single	
	TOPOLOGY: Illiear MOLECTILE TYPE: CDNA	
, us-0	ICAL: N	
Alig	Scores:	
Pred.	0.0046 Length:	
Perc	t Similarity: 31.21% Conservative:	
Query DB:	3.36%	
us-c	US-09-720-086-7 (1-912) x US-08-759-873-1 (1-3014)	

53 ArgLysArgLysHisProProValGluSerGlyAspThrProLysAspProAla----- 70

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368 AlaIleTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProValCys 387
                                                                                                                                                                                        749 GCCCGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 IleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTrpGlu 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaAlaGluThrLeuProGluAlaSerArgAlaValGlu-----AsnGlyCysCys 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCGAGGTCGGATCCCCACTGCTGTCGCCCAGCCGCAGGTCCGTTCCCGGGGAGCCAG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProGluGluGlySerProAlaGlyGlyGlnLysGlyGlyAlaProAlaGluGlyGluGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCC-------CTCCTCCCTGGAGACGGGGAGGAGAAAAGGGGGAGTCCAGTCGTC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerGlyAlaSerGluLeuLeuPro---AsnGlyAspLeuGluLysArgSer------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VallleSerLysSerProSerMetAlaGlnAsp 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----CTGGACAGTGTCTTGGACACTCTGTTGGCGCCCTCAGGTCCCGGGCAGAGCCAA 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTyrTyr 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrProLysGluGlyArgGlyAlaProAlaGluAlaGlyLysGluGlnLysGluThrAsn 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GGGACGGCAGCTGCCCATAÄÄGTGCTGCCCCGGGGCCTGTCA-----CCA 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---AGTCCCCCAGAAAAGGACAGCGGACTG---------
                                                 TCT-----GAGAGCCCTCACTGGTCCGGGGCCCCAGTGAAGCCGTCTCCGCAGGCC
                                                                                 SerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLys 367
                                                                                                                                                                                                                                                                                                                                                                                                                            ProThrAspProAlaSerProThrValAlaThrThrProGluProValGlySerAspAla 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------CCCAGCCCTCCCGCCTGCGAGGTCACCAGCTCTTGGTGCCTGTTTGGC 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTTCT------
                                                                                                                    -----CAGCTGCTCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GluProGln 100
                                                                                                                    772
                                                                                                                                                                                      754
                                                                                                                                                                                                                                                                                          307
                                                                                                                                                                                                                                                                                                                             703
                                                                                                                                                                                                                                                                                                                                                                                               667
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Bb 624 GCTGGGGTGAGGTTGAGGAG. 844
GCTGGGGTGGAGGTTGAGGAG ### ### ### ####

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373 GCTCAAGAGGGAGCTGGAGGCCAAGGCCGGAGAGCTGGCCCG------CGC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 GluProGlnProGluGluGlySerProAlaGlyGlyGlnLysGlyGlyAlaProAlaGlu 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 GCAGGAGGCCCTGAGCACAGAGCAGAGCAAGTCGGAGCTGAGCTCACGGCTGGACAC 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            577 GACCCGGGAGCAGCAGCCCAGCTCCCAGGAGCAGGCGAGTTGCAGGG----CCGGCTGGC 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 GlyProGlyAspThrSerSerSerAlaAlaGluArgGluGluAspArgLysAspGlyGlu 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 GluGlnGluGluProArgGlyLysGluGluArgGlnGluProSerThrThrAlaArgLys 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 ValGlyArgProGlyArgLysArgLys------His 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 ProProValGluSerGlyAspThrProLysAspProAlaValIleSerLysSerProSer 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: CDNA for Huntington-interacting protein
                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
TITLE OF INVENTION: Huntington's Disease Gene NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSE: Oppedahl & Larson
STREET: PO Box 5270
CITY: Frisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-720-086-7 (1-912) x US-09-085-199B-6 (1-3251)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.0051
166.00
31.74%
20.82%
3.36%
                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-085-199B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
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රි සි	Oy 118 GlyGluGlyAlaAlaGluThrLeuProGluAlaSerArgAla Db 634 AGAGAGGATCTCAGGAGCAGGGCTGCGGCAAGGAAGGACTGAAGAGAGAG	thrLeuProGluAlaSerArgAla 131 :: SCTGCTGGACGAGCAGTTCGCAGT 691
ò	132	14
QO	 694 GTTGCGGGGCGCTGCT	 cctgcaggatgccgtgag
λõ	Oy 148 GluAlaGlyLysGluGlnLysGluThrAsnIleGluSerMetLysMetGluGlySerArg	<pre>SerMetLysMetGluGlySerArg 167 :::::: ;;;</pre>
Q	745	CTCCCCAGACTACCTGGTGAGCAG 804
ò	Oy 168 GlyArgLeuArgGlyGlyLeuGlyTrpGluSerSerLeuArgGln-	
q ₀	805	TGCCGTGAGCACCCTGGAGGAGGG 846
ò	Oy 183ArgProMetProArgLeuThrPheGlnAlaGlyAspProTyrTyrIleSerLysArg	AspProTyrTyrlleSerLysArg 201
qq	847	ccccrcarcaccacccc 905
ò	Qy 202 LysArgAspGluTrpLeuAla-ArgTrpLys	oLys 211
QO	906	SCGGTGCCACCTCGCACCTGGCTC 965
δ	212	WalileAlaGlyMetAsnAlaVa 227
qq	Db 966 CCACCGACCCTGCCGACCGCTCATAGACACCTGCAGGGGGGGG	GGAGTGCGGGCCCGGGCTCTGG 1025
ò	Qy 227 lGluGluAsnGlnGlyProGlyGluSerGlnLy8ValGluGluAlaSerProProAlaVa	GluGluAlaSerProProAlaVa 247
qq	1026	GCACATGCAGGCCAGCTGGTGC 1085
ò	Qy 247 lGlnGlnPro	ThrAspProAlaSerProThrVa 258
qq	1086	
ò	Qy 258 lAlaThr	260
qq	Db 1146 TGCGGCAGGAGGAGCTGGGGCCGTGGTCGACAAGGAGGATGGCGGCCACATCCGCAGCCA	GATGGCGGCCACATCCGCAGCCA 1205
ò	261	ThrProGluProValGl 266
qa	Db 1206 TTGAAGATGCTGTGCGGAGGATTGAGGACATGATGAACCAGGCACGCCACGCCAGCTCGG	
ò	Oy 266 ySerAapAlaGlyAapLysAanAl	AspLysAsnAl 274
q	1266	CTGCACAGACCTGATGAAGGCTA 1325
ò	Qy 274 aThrLysAlaGlyAspAspGluProGlu-TyrGluAspGlyArgG	ProGlu-TyrGluAspGlyArgG 289
qq	1326	GGAGATCGTGGAGGCGCAGGG 1385
δ	289	gGlyPheSerTrpTrpProGlyA 309
QQ	1386	AACTCGCGCTGGACCGAAGGCC 1439
ογ	Oy 309 rglleValSerTrpTrpMetThrGlyArgSerArgAlaAlaGluG	irGlyArgSerArgAlaAlaGluG 324
q	1440	ACAGCTGGTGGAGGCAGCTGAC- 1498
δλ	Qy 324 lyThrArgTrpValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysL	ieSerValValCysValGluLysL 344
qq	1499	GCTCATCGTCTGCTCCCACGAGA 1553
ò	Oy 344 euMetProLeuSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProM	.nAlaThrTyrAsnLysGlnProM 364
qq	1554	GGTGAAGGCCAACAAGCACAGCC 1613
Oy	Qy 364 etTyrArgLysAlalleTyrGluValLeuGlnV	375
qa	1614	CAATGAGAGGGCTGCCAATGTGG 1673

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US-08-814-095-7/c
; Sequence 7, Application US/08814095
; Patent No. 6025183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/814,095
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1944 TGGCCCAGAAGCCC 1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1788 TGGAGCTGGAGAAGACGCTGGAGGCTGAACGCATGCGGCTGGGGGAGTTGCGGAAGCAAC 1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1728 TCTCCGGCCTGTCCCTCATCAAGCTGAAGAAGCAGGAGATGGAGACGCAGGTGCGTGTCC 1787
                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including
DESCRIPTION: promotor, ACHE gene and A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                          HYPOTHETICAL: NAME OF THE PROPERTY OF THE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
POSITION IN GENOME: CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375
                                                                                                                                                                                                                                                                                                                                                   LENGTH: 35060 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Farmington Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ysGluValTyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProProProP 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTACGTGCTGGCTGGGGCATCAGGC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hrAla-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roAlaLysLysPro 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alAlaSerSerArgAlaGlyLysLeuPheProValCysHisAspSerAspGluSerAspT
|||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: KOHN & ASSOCIATES 30500 No. 6025183thwestern Highway, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soreq, nerman
Zakut, Haim
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                                                                        Homo sapiens
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LOCATION: 27005..27274
IDENTIFICATION METHOD: e
OTHER INFORMATION: /evid
OTHER INFORMATION: /gene
OTHER INFORMATION: /numb
FEATURE:
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OTHER INFORMATION:
OTHER INFORMATION:
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FEATURE:
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OTHER INFORMATION:
FEATURE:
NAME/KEY: terminato
LOCATION: 28129..28
                                                                                                                                                                                         NAME/KEY: exon
LOCATION: complement (34528..34895)
OTHER INFORMATION: /function= "arserother information: gene"
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 1
FEATURE:
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NAME/KEY:
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NAME/KEY: promoter
LOCATION: 4089..22464
OTHER INFORMATION: /function= "ACHE Promotor"
OTHER INFORMATION: /standard_name= "ACHE Promotor"
FEATURE:
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NAME/KEY:
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LOCATION:
                              LOCATION: complement (33779..33963)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
                                                                                                                    NAME/KEY: exon
LOCATION: complement (34092..34358)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 2
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OTHER INFORMATION: /ge
OTHER INFORMATION: /ge
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IDENTIFICATION METHOD:
OTHER INFORMATION: /evi
OTHER INFORMATION: /ger
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OTHER INFORMATION: /fu
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                                                                   NAME/KEY: exon
LOCATION: comp
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27255..28007
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/gene= "ACHE"
/number= 6
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/evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 5
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/gene= "ACHE"
/number= 4
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/gene= "ACHE"
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24110)"
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/gene= "ACHE"
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
LOCATION: complement (33493..33591)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 4
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
FRATURE:
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OTHER INFORMATION: /gene= "ARS"
OTHER INFORMATION: /number= 16
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
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OTHER INFORMATION: /number= 7
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 11
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
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NAME/KEY: exon
LOCATION: complement (30470..30626)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
                                                                                                                 LOCATION: complement (33297..33408)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 5
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 8
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Best Local Similarity:
Query Match:
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24257 CCCGCAGCCCCCCCCCCCACGCTCACCAGCA--------GCTCTGCAT 24216
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                                                                                                                                                                                                                                                                                      24176 AGAGGAGAAGAAGAAGGAGTGGGAAAGCCA----GGGAAGGCGTGTGCAGCAGACACT 24123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23915 AGGCC---AGCGGGCAGGAGAGAGAATCAGGCAGACACCCATATCCAGACAAATGC 23859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23798 GGAACTGGGCCCGGGCCCA------GCTCGTGCAGTGAGGCCACAGAAGCCTCA 23751
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                                                                                                                                                                                                                                                    89 ProAsnGlyAspLeuGluLysArgSerGluProGlnPro-----GluGluGlySer 105
                                                                                                                                                                                                                                                                                                                                                        106 ProAlaGlyGlyGlnLysGlyGlyAlaProAlaGluGlyGluGlyAlaAla-GluThrLe 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 rgGlyAlaProAlaGluAlaGlyLysGluGlnLysGluThrAsnileGluSerMetLysM 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 erLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTyrTyrIleS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 erLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLysLysAlaL 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 al-GluGluAlaSerProProAlaValGlnGlnProThrAgpProAlaSerProThrVal 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 ysValileAlaGlyMetAsnAlaValGluGluAsnGlnGlyProGlyGluSerGlnLysV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 AlaThrThrProGluProValGlySerAspAlaGlyAspLysAsnAlaThrLysAlaGly 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279 AspAspGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeuValTrpGly 298
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                                                                                                                                                 69 ProAlaValileSerLysSerProSerMetAlaGlnAspSerGlyAlaSerGluLeuLeu 88
                                                 49 GlyArgProGlyArgLysArgLysHisProProValGluSerGlyAspThrProLysAsp 68
US-09-720-086-7 (1-912) x US-08-814-095-7 (1-35060)
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RESULT 10
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GENERAL INFORMATION:
APPLICANT: WRIGHT, Jim A.
APPLICANT: YOUNG, Aiping H.
APPLICANT: LEE, Yoon S.
TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR II ANTISENSE OLIGONUCLECTIDE
TITLE OF INVENTION: SEQUENCES AND METHODS OF USING SAME TO MODULATE CELL
TITLE OF INVENTION: GROWTH
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                                                                                                                                                                                                                                                                                                                                                                                                  ArgGluValLeuMetCysGlyAsnAsnAsnCysCysArgCysPheCysValGluCysVal
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 4350
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CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 60/082,791
EARLIER FILING DATE: 1998-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysGluThrAsnIleGluSerMetLys---MetGluGlySerArgGlyArgLeuArgGly 172
                                                                                                                                                                                                                                                                                     AsnGlyCysCysThrProLysGluGlyArgGlyAlaProAlaGluAlaGlyLysGluGln 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCAGGACTTCTGGGGACCAGCCACTGTCCCCA---
                             GluAlaGluLysLysAlaLysValIleAlaGlyMetAsnAlaValGluGluAsnGlnGly
                                                               GGGGGGTTTAATTTGGTTTCTGAGCGCATAAAG-
                                                                                         GlyAspProTyrTleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArg
                                                                                                                            TCTCCAGGCTGGCTTCGTGCGTTCTTGTCACTGCCCCCC---TGTTACATGGGG
                                                                                                                                                       GlyLeuGlyTrpGluSerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAla 192
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Indels:
-GGAAA-AATGCCCCAAGAAACAAAGAGGGG
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בפונה סדייודים באיסספ		
Alignment Scores: 0.0401 Pred. No.: 0.0401 Score: 161.00	Oy 513 -MetCygGlnAsnCysLysAsnCysPheLeuGluCysAlaTyrGlnTyrAspAspAspGl 532 :::	- u
COCATION: 237.7037 COTHER INFORMATION: /standar US-08-949-386-23	Qy 494 sIleSerCysGlySerLeuAsnValThrLeuGluHisProLeuPheValGlyGly 512	
line PE: I	Qy 474 gThrArgGluArgLeuValTyrGluValArgGlnLysCy8ArgAsnIleGluAspIleCy 494 :::	
r. R	Qy 461	
016	Oy 446 AlaAlaTyrAlaProProProProAlaLys	
ATTORNEY/AGENT INFORMATION: NAME: Seidman, Stephanie L. REGISTRATION NUMBER: 33,775	<pre>Oy 426 GluGluLysAbnProTyrLysGluValTyrThrAspMetTrpValGluProGluAla 445</pre>	
; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: 08/105, ; FILING DATE: 11-AUG-1993	:::	
; FILING DATE: 11-AUG-1994 ; APPLICATION NUMBER: 08/149,	Db 2462 GCTCACGCTGCGGGGCCGTGGGGACACGCGCCAAGGAGGCCAGCCTCACAAGGGCATCT 2403 Ov 407 IlaGluTrnalalalanGlvGlvPheGlnProSerGlvProfvSGlvLanGluProPro 425	
CLASPITICATION: PRIOR APPLICATION: APPLICATION NUMBER: US/08/2	387 CysHisAspSerAspGluSerAspThrAlaLysAlaValGluValGlnAsnLysBroMet	-
CURRENT APPLICATION DATA: , APPLICATION NUMBER: US/08/9 , FILING DATE:	Qy 367 LysAlaileTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProVal 386	
ER: IBM ING SYST	2531 CACTCTGGCTGGGCCAACACA	_
ZIP: 92101 ; COMPUTER READBLE FORM: MEDITM TYPE: Flormy disk	Db 2582GGCATGTCTGCTCAGCTACCGGCCATCTCCAATGTGGCCAAACTCCTTCCT	
;; ≝	331 PheGlyAspGlyLysPheSerValValCysValGluLysLeuMetPro	-
CORRESSE: ADDRESSEE: Brown, Martin, F. STREET: 1660 Union Street	OY SIL VALSELLIPIIEMELINGLYPRISELFINGALACTURINGLIPULALINGLIPULAL SSU	_
; TITLE OF INVENTION: METHODS ; NUMBER OF SEQUENCES: 38	2660 TCCCTAGGTGTGCTCCGGTGGGGGGGTCCCCAAGATCTTCCTTCCAGG	
MCCUE, Ar Gillespie IVENTION:	291 GlylleGlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrpTrpFroGlyArglle :::	_
	Db 2675	_
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386-23	254 AlaSerProThrValAlaThrThrProGluProValGlySerAspAlaGly	-
Db 1915GTC	OY 235 GIUSELCIMANDAVAICTUGIUALESEEFOTTE FLOAGAVAICTUGICALE COMMANDE 253 DD 2795 AACTECCCCCCCAGCCCCCACTGCCCCCACCCCACCCCCCCCAGACTTCCCA 2736	
Qy 572 aGlnAlaAlaIleLysGluAspPrc	2855 CTGCTGTCAATCCTCCTGACTTTTCCATCCAAAATCTCCCGGGACCACTTCCTACCCCAG	
Db 1964 IGTGTGCTGCATGCGTGTGCGTGCGTGCGTGCTGCGTGCGT	Qy 233ProGly 234	
2024 GCATGAGTGTGTGTGTGTGT	Db 2915 GAATAGATCAATTGACATGAAATTTGGGGGTTCCTAATTTCTCTATGTAATTCTGCAAGT 2856	
532	Qy 232 232	

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/alGluCysValAspLeuLeuValGlyProGlyAlaAl 572
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PALCIUM CHANNEL COMPOSITIONS AND
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Matches: 165
Conservative: 73
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399	- da	3449 CATGANGAACAACAAGCTGGCCACCGCGGAGTCGGCCGCTCCCCACGGCAGCCTTGGCCA	
62	Qy	Ov 293 GlvGluLeuValTrpGlvLvsLeuArgGlvPheSerTrpTrpPro 307	
393	ф	3389 CCGGCCAATCCAGCAGGACCTGGGCCGCCAAGACCCACCC	
19	ν,	273 AsnAlaThrLysAlaGlyAspAspGluProGluTyrGluAspGlyArqGlyPheGlyIle	
388	da	3362AACCAC	
5	Qy	253 ProAlaSerProThrValAlaThrThrProGluProValGlvSerAsnAlaGlvAsnIva	
387	מם	3317GCGGAGGCATCGGAGGAAAGAAGAAACCAGGGCTCCCGGGGTCCC	
57	Qy	233 ProGlvGluSerGlnIvsValGluGluAlaSerProProAlaValGlnGlnDroThrAsn	
387	Db		
55	γQ	218 AlaTvsValTlealaGlvMorAsnalaValGluGluAsnGlnGlv	
386	ממ	bb 3206 CCGGGGCGAGGAGGGCGAAGGGGCCCCGACGGAGGGGCGAGCGCAAGGAGAAG 3259	
53	Qy	31/3 GAGGGCGCGCACCGCGA	
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51	Qy	78 Serserieilarrollarromer Dromer Dromer Dromer Drome	
385	מם	Qy 158 IleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTrpGlu 177	
49	Qy	3033 GERGGGGERGERGERGERGERGERGERGERGERGERGERG	
384	שמ		
47	γQ	149 Alacivivecincinivecinthraen	
378	da	3014	
45	Qy	Qy 133 GluAsnGlyCysCysThrProLysGluGlyArqGlyAlaProAlaGlu 148	
372	Db	Db 2969 GGGCAGCCTGGAGCAACCCGGGTTCTGGGAGGGCGAGGCCGAGCG 3013	
44	ý	Oy 113 GlyAlaProAlaGluGlyGluGlyAlaAlaGluThrLeuProGluAlaSerArgAlaVal 132	
366	מס	2918 GCTGAGCCGGGAGGACCCTACGGCCGCGAGTCGGACCACCACGCCCGGGA	
42		Qy 93 LeuGluLysArgSerGluProGlnProGluGluGlySerProAlaGlyGlyGlnLysGly 112	
362	ad d		
40	УО	76 ProSerMetalaClnAsnSerClvAlaSerCliT.enT.enProAsnClvAsn	
358	рь	2813 GGACTTCCTCAGGAAACAGGCCCGCTACCACGATCGGGCCCGGGA	
38	Qy	56 LysHisProProValGluSerGlyAspThrProLysAspProAlaValIleSerLysSer	
356	. ეხ	2753 CAACAAGAGCCGGGCCGAGCCCACCGTGGACCAGCGCCTGGGCCAGCAGCAGCGCCGA	
36	Qy	38 AraGlnGluProSerThrThrAlaAraLvsValGlvAraProGlvAraLvsAra	
354	מס	2696 GACGCACTTGGACCGGCCGGTGGTGGTGGACCCGCAGGAGAACCGCAACAACAACAC	
34	γo	22 AspArgivsAspGlvGluGluGluGluProArgGlvLvsGluGlu	
353	Db.	2636 AATGGACCCGGACGAGCGTGGAAGGCTGCCTACACGCGGCACCTGCGGCCAGACATGAA	
32	Qy	7 SerGlvProGlvAs	
350	σb	09-720-086-7 (1-912) v MC-09-040-386-23 (1-7701)	
30	Qy	Best Local Similarity: 20.52% · Mismatches: 234 Query Match: 3.26% Indels: 334 DB: Gans: 41	

629GluLysArgLysProIleArg	P &	
616 GluPheAspProProLysValTyrProProValProAla	P &	
596 ArgArgArgGluAspTrpProSerArgLeuGlnMetPhePheAlaAsnAsnHisAspGln	음	
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3785 CCACACCGTACAAGTGAACAAAAACGCCAACCCAGACCCACTGCCAAAAAAAA	מם	
456 LysProArgLysSerThrAlaGluLysProLysValLysGluIleIleAspGluArgThr	Qy	
3725 TGCCAGGAAACCCGACCACACCACAGTGGACATCCCCCCAGCCTGCCACCCCCCCC	dd An	
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428 GluLysAsnProTyrLysGluValTyrThrAspMetTrp	ž &	
3626CAACCCGGGGAACCCATCCAATCCCGGCCCCCCAAGAC	Вb	
408 GluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGluProProGluGlu 	9	
3581 CATGGCCACCAACCCCCAGAACGCCGCCGCCGGACGCCCAA	рb	
388 HisAspSerAspGluSerAspThrAlaLysAlaValGluValGlnAsnLysProMetIle	Qy	
3563	gg .	
368 AlaIleTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProValCys	Q	
3545	ממ	
348 SerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLys	γQ	
3536GATGGGAAA	Дb	
328 ValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLeu	8	
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308 GlyArgIleValGerTrpTrpMetThrGlyArgSerArgAlaAlaGluGlyThrArgTrp	8	

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4058 ACCTCGGAACAACGTGCTGCGATACTTTGACTACGTTTTTACAGGCGTCTTCACCTTT-- 4115
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                                                                                                                       4116 ----GAGATGGTGATCAAGATGATGA 4138
636 ------ValLeuSerLeuPheAspGlyIleAlaThrGlyLeuLeuValLeuLy 651
                                                                                  651 sAspLeuGlyIleGlnValAspArgTyrIleAlaSerGluValCysGluAspSerIleTh 671
                                                                                                                                                               671 rValGlyMetValArgHisGlnGlyLysIleMetTyrValGlyAspValArgSerValTh 691
                                                                                                                                                                                                                                               691 rGlnLysHis1leGlnGluTrpGlyProPheAspLeuVal1leGlyGlySerProCysAs 711
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APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Miliams, Mark
APPLICANT: Miliams, Mark
APPLICANT: Miliams, Mark
APPLICANT: Gillespie, Alison
APPLICANT: Feldman, Daniel
APPLICANT: Feldman, Daniel
APPLICANT: Brenner, Robert
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Brown, Martin, Haller & McClain
1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE:
CLASSIPICATION: 435
PRIOR APPLICATION NUMBER: 08/404,950
FILING DATE: 13-MAR-1995
FILING DATE: 7-NOV-1994
FRIOR APPLICATION NUMBER: 08/336,257
FILING DATE: 7-NOV-1994
PRIOR APPLICATION NUMBER: 08/314,083
FILING DATE: 28-SEPT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/450,562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/08450562
Patent No. 6096514
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: 4-APR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08/311,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UMBER: 08/290,012
11-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 23-SEPT-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    San Diego
: California
XY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                         4293 GTGCTACGAC 4302
                                                                                                                                                                                                                                                                                                                                                                                                            722 yLeuTyrGlu 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-450-562-23
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2636 AATGGACCGGACGAGGCTGGAAGGCTGCCTACACGCGGCACCTGCGGCCAGACATGAA 2695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 Asp-----ArgLysAspGlyGluGluGluGluHroArgGlyLysGluGlu 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 SerglyProglyAspThr-----SerSerSerAlaAlaGluArgGluGlu 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: /standard_name= "Alpha-1A-2" US-08-450-562-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-720-086-7 (1-912) x US-08-450-562-23 (1-7791)
                                                                                                                                                                                                                                APPLICATION NUMBER: 07/914,231
FILING DATE: 13-UULY-1992
PRIOR APPLICATION NUMBER: 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION NUMBER: 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA: PCT/US92/06903
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA: 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION NUMBER: 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA: 30-NOV-1990
PRIOR APPLICATION DATA: 07/603,751
FILING DATE: 08-NOV-1990
PRIOR APPLICATION DATA: 07/82,384
FILING DATE: 07-REB-1990
PRIOR APPLICATION DATA: 07/82,384
FILING DATE: 07-APR-1989
PRIOR APPLICATION DATA: 07/176,899
FILING DATE: 07-APR-1989
PRIOR APPLICATION DATA: 07-APR-1989
PRIOR APPLICATION NUMBER: 07/176,899
FILING DATE: 04-APR-1989
PRIOR APPLICATION NUMBER: 07/176,899
FILING DATE: 04-APR-1989
PRIOR APPLICATION NUMBER: 03,779
REPERENCE/DOCKET NUMBER: 6362-519812
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: 08/193,078
FILING DATE: 07-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/149,097
FILING DATE: 5-NOV-1993
PRIOR APPLICATION NUMBER: 08/105,536
FILING DATE: 1-AUG-1993
PRIOR APPLICATION NUMBER: 08/105,436
FILING DATE: 1-AUG-1993
PRIOR APPLICATION NUMBER: 07/914,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (619) 238-0999
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
LENGTH: 7791 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161.00
29.60%
20.52%
3.26%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237..7037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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;		368 AlaIleTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProValCys 387	γQ
691	Q ;	3545 3562	90
671	B 8	348 SerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLys 367	Ş
4116	ДЪ		90
651	જ	ValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLeu	Ś
4058	φa	308 GlyArgIleValSerTrpTrpMetThrGlyArgSerArgAlaAlaGluGlyThrArgTrp 327	유 성
636	S	3449 CATGAAGAACAAGCTGGCCACCGCGGAGTCGGCCGCTCCCCACGGCAGCCTTGGCCA 3508	Db
5000	ş	293 GlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrpTrpPro 307	8
3938	da da		Db ·
616	δ	AsnAlaThrLysAlaGlyAspAspGluProGluTyrGluAspGlyArqGlyPheGlyIle	ર !
3881	Db	253 ProAlaSerProThrValAlaThrThrProGluProValGlySerAspAlaGlyAspLys 272	₹ 8
596	γ2	GCGGAGGCATCGGAGGAGGAAACCAGGGCTCCGGGGTCCC	55
3872	Дb	ProGlyGluSerGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAsp	g QV
576	Qy	GCACCGGCATGGCGCCACCCACGTACGAGGGGGACGCGCGGAGGGAGGACAAGGA	g D
3871	B	AlabysValileAlaGlyMetAsmAlaValGluGluAsmGlnGly	. 8
556	S S	CCGGGGCGAGGGCGAGGGCGAGGGCCCCGACGGGGGCGAGCGCAGGAGAAG	, B
3860	ᅡ	gGlu	ş
536	S S	3173 GAGGGCGCGCACCGCGA	В
3859	뫄	SerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTyrTyr	. S
516	δ		Db
3854	υь	IleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTrpGlu	Ş. Ş
496	S S	GCAGGGGGCAGCAGGAGAGCCGCAGCGGGTCCCCGCGCACGGGCGCGGGACGGGAGCA	Дb
3845	8	AlaGlyLysGluGlnLysGluThrAsn	Ş
476	2	AGGCAAGGCCGGGACCCCCACCGGAGGCACGTGCACCG	Вb
3785	ਰੂਹ	GluAsnGlyCysCysThrProLysGluGlyArgGlyAlaProAlaGlu	Ş
456	Q {	2969 dddcadddiddaddaacccddgritdiddaggagagacaaggcddaddd 3013	рь
3 7 7 1 1 1 1	3 5	113 GlyAlaProAlaGluGlyGluGlyAlaAlaGluThrLeuProGluAlaSerArgAlaVal 132	γO
3665	dα		Db '
428	Q		Ş
3626	дb	:::	Db .
408	ν	ProSerMetAlaGlnAspSerGlvAlaSerGluLeuLeuProAsnGlvAsp	Q :
3581	Db	56 LysHisProProValGluSerGlyAspThrProLysAspProAlaValIleSerLysSer 75	음 성
388	8		g
3563	dd	ArgGlnGluProSerThrThrAlaArgLysValGlyArgProGlyArgLysArg	8

Qy	Дb	ργ	타	Ş	Db &	2	ş 8	망	ð	Dβ	Ŋ	탕	Ş	В	Ş	DЬ	á	뮹	Ş	뮹	Ş	윱	Q	D d	Ş	망	Q	D	Ş	뮰	ογ	망	Ş	Db
691	4139	671	4116	651	4058	y 6	3998	3938	616	3881	596	3872	576	3871	556	3860	536	3859	516	3854	496	3845	476	3785	456	3725	44	3665	428	3626	408	3581	388	3563
rGlnLysHisIleGlnGluTrpGlyProPheAspLeuValIleGlyGlySerProCysAs 711	CCTGGGGCTCGTCCTGCÁTCÁGGGTGCCTÁCTTCCGTGACCTCTGGAATATTCT 4192	rValGlyMetValArgHisGlnGlyLysIleMetTyrValGlyAspValArgSerValTh 691	GAGATGATGATGATGATGA 4138	sAspLeuGlyIleGlnValAspArgTyrIleAlaSerGluValCysGluAspSerIleTh 671		caigaicai dochaigageaghachteachteachteachteachteachteachteacht	GluLysArgLysProIleArg	CCCCCTTCGCCGCCTGTGCCATTACATCCTGAACCTGCGCTACTTTGAGATGTGCATCCT 3997	GluPheAspProProLysValTyrProProValProAla628	AGACGGCCTAAGCCAATGCCTCCCTATAGCTCCATGTTCATCCTGTCCACGACCAA 393	ArgArgGluAspTrpProSerArgLeuGlnMetPhePheAlaAsnAsnHisAspGln 615	CCGTGGGGA 3880	IleLysGluAspProTrpAsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeu 595	3871	ArgCysPheCysValGluCysValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAla 575	3871	TyrCysThrIleCysCysGlyGlyArgGluValLeuMetCysGlyAsnAsnAsnCysCys 555	3859	AsnCysLysAsnCysPheLeuGluCysAlaTyrGlnTyrAspAspAspGlyTyrGlnSer 535		SerCysGlySerLeuAsnValThrLeuGluHisProLeuPheValGlyGlyMetCysGln 515	AGAGAAGAA 385	ArgGluArgLeuValTyrGluValArgGlnLysCysArgAsnIleGluAspIleCysIle 495	CACACCGTCGTACAAGTGAACAAAAACGCCAACCCAGACCCACTGCCAAAAAAAA	LysProArgLysSerThrAlaGluLysProLysValLysGluIleIleAspGluArgThr 475	CCAGGAAACCCGACCACACCACAGTGGACATCCCCCCAGCCTGCCCACCCCCCCTCAA	ValGluProGluAlaAlaAlaTyrAlaProProProProAlaLys	::: ::: ::: ::: ::: ::: ::: ::: ::: ::	GluLysAsnProTyrLysGluValTyrThrAspMetTrp 440	CAACCCGGGGAACCCATCCAATCCCGGCCCCCAAGAC 366	luG	CATGGCCACCAACCCCCAGAACGCCGCCAGCCGCCGAACGCCCAA 3625	HisAspSerAspGluSerAspThrAlaLysAlaValGluValGlnAsnLysProMetIle 407	 CATGCTGGCCATCCCTGC 3580

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4234 -TCACTGGCAATAGCAAAAGGAAAAGACATCAACACGATTAAATCCCTCCGGAGTCCTCCGG 4292
------GGTAGCCTTTGCCT 4233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2636 AATGGACCCGGACGAGGCTGGAAGGCTGCCTACACGCGGCACCTGCGGCCAGACATGAA 2695
                                             711 nAspLeuSerIle-----LysGl 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 SerGlyProGlyAspThr-----SerSerSerAlaAlaGluArgGluGlu 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 Asp-----ArgLysAspGlyGluGluGluGluGluGluroArgGlyLysGluGlu 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEO Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/984,709A

FILING DATE: 02-DEC-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Seldman: Stephanie L.

REGISTRATION NUMBER: 33,779

TELECOMMUNICATION INFORMATION:

SEQUENCE CHARACTERISTICS:

LENGTH: 7791 base pairs
                                                                                                                                                                                                                         RESULT 13
US-08-984-709A-23
i Sequence 23, Application US/08984709A
; Patent No. 6320032
; GENERAL INFORMATION:
    APPLICANT: Williams, Mark E. APPLICANT: Harpold, Michael M. TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND TITLE OF INVENTION: METHODS
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Heller Ehrman White & MCAuliffe STREET: 4250 Executive Square, Suite 700
    CITY: La Jolla
    STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS

LOCATION: 237..7037

CTHER INFORMATION: /standard_name= "Alpha-lA-2"

US-08-984-709A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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4193 -CGACTTCATAGTGGTCAGTGGGGCCCT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0401
161.00
29.60%
20.52%
3.26%
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                                                                                                                                        722 yLeuTyrGlu 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No.
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đ	2696 GACGCACTTGGACCGGCCGCTGGTGGACCCGCAGGAGAACCGCAACAACAACAC 2752
ò	38 ArgGlnGluProSerThrThrAlaArgLysValGlyArgProGlyArgLysArg 55
Q	2753 CAACAAGAGCCGGGCCGGCCGAGCCCACCGTGGACCAGCGCCCTCGGGCAGCAGCGCGCCGA 2812
ò	56 LysHisProProValGluSerGlyAspThrProLysAspProAlaValIleSerLysSer 75
qa	2813 GGACTTCCTCAGGAAACAGGCCGCTACCACGATCGGGCCCGGGA 2857
ò	76 ProSerMetAlaGlnAspSerGlyAlaSerGluLeuLeuProAsnGlyAsp 92
qa	GGCGGGAAG
ò	93 LeuGluLysArgSerGluProGluProGluGluGlySerProAlaGlyGlyGlnLysGly 112
qq	2918 GCTGAGCCGGGAGGGACCCTACGGCCGGAGTCGGACCACCACGCCCGGGA 2968
ò	113 GlyalaProAlaGluGlyGluGlyAlaAlaGluThrLeuProGluAlaSerArgAlaVal 132
g	2969 GGGCAGCCTGGAGCAACCCGGGTTCTGGGAGGGCGAGGCCGAGCG 3013
ò	3 GluAsnGlyCysCysThrPro
qq	3014AGGCAAAGGCGGGGGACCCCCACGGAGGCACGTGCACCG 3052
ò	149 AlaGlyLysGluGlnLysGluThrAsn 157
g	3053 GCAGGGGGGAGCAGCAGAGCCGCAGGGGTCCCCGCGCACGGGCGGG
ò	158 IleGluSerMetLy8MetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTrpGlu 177
qq	3113 TCGACGTCATCGCGCCACCGCAGGCCCGGGGAGGAGGAGGTCCGGAGGACAAGGCGGAGCG 3172
ò	178 SerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTyrTyr 197
qq	3173 GAGGGGGGGCGCCGCGCGCGCGCGCGCGGCGGCGGCGGCG
ò	ArgGluAlaGluLy
qq	3206 CCGGGGCGGGGGGGGGGGGGGCCCCCGACGGGGGGGGGG
δ	218 AlaLysVal
qa	regeeetecagecae
ò	233 ProGlyGluSerGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAsp 252
QQ	3317GCGGAGGCATCGGAGGAGGAAGAGAACAGGCTCCGGGGTCCC 3361
ò	253 ProAlaSerProThrValAlaThrThrProGluProValGlySerAspAlaGlyAspLys 272
qq	3362AACCAC 3388
ò	273 AsnAlaThrLysAlaGlyAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIle 292
qq	3389 CCGGCCAATCCAGCAGGACCTGGGCCGCCAAGACCCACCC
ò	293 GlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrpTrpPro 307
qq	3449 CATGAAGAACAACAGCTGGCCACGGGGGTCGGCCGCTCCCCACGGCAGCCTTGGCCA 3508
ò	308 GlyArgIleValSerTrpTrpMetThrGlyArgSerArgAlaAlaGluGlyThrArgTrp 327
рр	3509
ò	328 ValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLeu 347
g	3536GATGGGAAA3544
ò	348 SerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLys 367
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691 4192	rValGlyMetValArgHisGlnGlyLysIleMetTyrValGlyAspValArgSerValTh ::: ::	671 4139	유 성
4138		4116	рь
671	sAspLeuGlyIleGlnValAspArgTyrIleAlaSerGluValCysGluAspSerIleTh	651	δ
4115	ACCTCGGAACAACGTGCTGCGATACTTTGACCTACGTTTTTACAGGCGTCTTCACCTTT	4058	B &
1 0	TIGGT CATTIGCCA THE TOTAL CATTIGCT CONTROL OF THE TOTAL CATTIGCT C	υ	? 5
i ü	GluLysArgLysProIleArg	62	\$ 8
3997	CCCCCTTCGCCGCCTGTGCCATTACATCCTGAACCTGCGCTACTTTGAGATGTGCATCCT	3938	B
628	GluPheAspProProLysValTyrProProValProAla	616	8
3937	AGACGGCCTAAGCCAATGCCTCCCTATAGCTCCATGTTCATCCTGTCCACGACCAA	3881	망
615	SerArgLeuGlnMetPhePheAlaAsnAsnHisAspG	596	80
3880	CCGTGGGGA	3872	망
595	1CysTyrMetCysGlyHisLysGly	576	γQ
3871		3871	B
575	CysPheCysValGluCysValAspLeuLeuValGlyProGlyAlaAlaGlnA	556	Ş
3871	GGAGGAAGAC	3860	Вb
555	TleCysCysGlyGlyArgGluValLeuMetCysGlyAsnA	536	ş
3859		3859	Дb
535	ysAlaTyrGlnTyrAspAspAspGlyTyrGl	516	ş
3859		3854	Дb
515	AsnValThrLeuGluHisProLeuPheVai	496	ş
3853	AA	3845	ф
495	GluArgLeuValTyrGluVa	476	δ
3844	ACCGTCGTACAAGTGAACAAAAACGCCAACCCAGAC		B 2
1 1		n N	?
455 3784	ValGluProGluAlaAlaAlaTyrAlaProProProProAlaLys	141 3725	B S
3724	NATAGCCTTATCGTCACCCAACCCCAGCGGCACCCAGACCAATTCAGCTAAGAC	3665	셤
440	AsnProTyrLysGluValTyrThrAspMetTrp	428	δ
3664	GIUTTPAIALEUGIYGIYPNEGINPYOSETGIYPTOLYSGIYLEUGIUPTOPYOGIUGIU	3626	유 성
on.	CCACCAACCCCAGAACGCCGCCAGCCGCCGGACGCCCAA	· œ	g
407	SerAspGluSerAspThrAlaLysAlaValGluValGlnAsnLysProMetIle		\$
3580	CATGCTGGCCATCCCTGC	3563	gg
387	euPheProValCys	368	8

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; Sequence 23, Applicat
; Patent No. 6387696
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/404,950
FILING DATE: 13 MAR-1995
APPLICATION NUMBER: 08/336,257
FILING DATE: 7-NOV-1994
PRIOR APPLICATION NUMBER: 08/314,083
APPLICATION NUMBER: 08/314,083
FILING DATE: 28-SEPT-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/311,363
FILING DATE: 23-SEPT-1994
CLASSIFICATION 435
CLASSIFICATION 435
CLASSIFICATION 435
                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/290,012

FILING DATE: 11-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/223,305

FILING DATE: 4-APR-1994

CLASSIFICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/193,078

APPLICATION NUMBER: 08/193,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 92101
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: McCue, Ann
APPLICANT: Gillespie, Alison
APPLICANT: Feldman, Daniel
APPLICANT: Feldman, Daniel
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: 08/149,097
FILING DATE: 5-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,536
FILING DATE: 11-AUG-1993
                                                                               APPLICATION NUMBER: 08/193,000
FILING DATE: 07-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4293 GTGCTACGAC 4302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4234 -TCACTGGCAATAGCAAAGGAAAAGACATCAACACGATTAAATCCCTCCGAGTCCTCCGG 4292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4193 - CGACTTCATAGTGGTCAGTGGGGCCCCT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1660 Union
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yLeuTyrGlu 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nAspLeuSerIle-----LysGl 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rGlnLysHisIleGlnGluTrpGlyProPheAspLeuValIleGlyGlySerProCysAs 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08450272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harpold, Michael
Ellis, Steven
Williams, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brown, Martin, Haller & McClain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTAGCCTTTGCCT 4233
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2636 AATGGACCCGGACGAGGAGGCTGGAAGGCTGCCTACACGCGGCACCTGCGGCAGAACATGAA 2695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2696 GACGCACTTGGACCGGCCGCTGGTGGACCCGCAGGAGAACCGCAA---CAACAACAC 2752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2753 CAACAAGAĞCCGGCCGGCCGACCCACCGTGGACCAGCGCCTCGĞCCAGCAGCGCGCGĞA 2812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2858 CCCCAGCGGCTCGGCGGCCTGGACGCACGGAGGCCCTGGGCGGGAAGCCAGGAGGCCGA 2917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2918 GCTGAGCCGGGAGGGACCCTACGGCGGGAGTCGGACCACCA-----CGCCCGGGA 2968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2969 GGGCAGCCT-----GGAGCAACCCGGGTTCTGGGAGGCCGAGGCCGAGCG--- 3013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 LeuGluLysArgSerGluProGluProGluGluGlySerProAlaGlyGlyGlnLysGly 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 GlyAlaProAlaGluGlyGluGlyAlaAlaGluThrLeuProGluAlaSerArgAlaVal 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 Asp------ArgLysAspGlyGluGluGluGluGluProArgGlyLysGluGlu 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 ArgGinGluProSerThrThrAlaArgLys-----ValGlyArgProGlyArgLysArg 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 LysHisProProValGluSerGlyAspThrProLysAspProAlaValIleSerLysSer 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 ProSerMetAlaGlnAspSerGlyAlaSerGlyLeuLeu-----ProAsnGlyAsp 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 SerGlyProGlyAspThr-----SerSerSerAlaAlaGluArgGluGlu 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 237..7037
CTHER INFORMATION: /standard_name= "Alpha-1A-2"
US-08-450-272-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-720-086-7 (1-912) x US-08-450-272-23 (1-7791)
                  FILING DATE: 13-JULY-1992
CLASSIPICATION NUMBER: 07/914,231
FILING DATE: 13-JULY-1992
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 10-APR-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/869,354
FILING DATE: 14-AUG-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/745,206
FILING DATE: 15-AUG-1991
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
RELECOMMUNICATION INFORMATION:
TELEFANCE: (619) 238-0999
TELEFANCE: (619) 238-0999
TELEFANCE: (619) 238-0962
INFORMATION FOR SEQ 1D NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 7791 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.0401
161.00
29.60%
20.52%
3.26%
PRIOR APPLICATION DATA:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Š	133 GIUABNGIYCYSCYSTREPE	148
ΩP	Db 3014AGGCAAGGCCGGGGACCCCCACCGAAGGCACGTGCACG	ACCG 3052
ò 6	OY 149 AladlytysGludInLysGluThrAsn	157
ò	158 lleGluSerMetLysMetGluGlySerAraGlyAraLeuAraGlyGlyLeuGly	177
연	113 TCGACGTCATCGCGCGCCCCGCAGGCCCGGGGAGGAGGAGGAGGAGGAGG	
ò	Oy 178 SerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaglyAspProTyrTyr	rTyr 197
Q	3173	CGGC 3205
ò	198	6Lys 217
QQ	3206 CCGGGGCGAGGGCGAGGCGAGGCCCCGACGGGGGC	GAAG 3259
ò	Qy 218 AlaLysVal	nGly 232
QQ	3260	AGGA 3316
ò	Qy 233 ProGlyGluSerGlnLysValGluGluAlaSerProProAlaValGlnGlnBroThrAsp	rAsp 252
අු	3317	3361
ò	Oy 253 ProAlaSerProThrValAlaThrThrProGluProValGlySerAspAlaGlyAspLy	pLys 272
엄	3362TGTGTCGGGCCCCAACCTGTC	-AACCAC 3388
Ø	2y 273 AsnAlaThrLysAlaGlyAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIle	yile 292
임	3389	ACAA 3448
ò	293	pPro 307
OP	3449	GCCA 3508
ò	308 GlyArgileValSerTrpTrpMetThrGly	gTrp 327
අු	3509	A 3535
ò	2y 328 ValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProL	oLeu 347
q	3536	3544
ò	2y 348 SerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLys	gLys 367
q	3545	3562
ά	368 AlaileTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPhePro	1Cys 387
qa	3563CATGCTGGCCAT	CCCTGC 3580
ò	388	tile 407
q	3581	3625
ò	3y 408 GluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGluProProGluGl	uGlu 427
QQ	3626	AGAC 3664
ò	2y 428 GlubyaAsnProTyrLysGluvalTyrThrAspMetTrp	440
q	3665	AGAC 3724
ò	2y 441ValGluProGluAlaAlaAlaTyrAlaProProProProAlaLys	aLys 455
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                                                                                                        US-08-949-386-22
                                                                                                                          RESULT 15
                                                                                                                                                        8
                                                           Sequence 22, Applicat Patent No. 6090623
GENERAL INFORMATION:
                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3859
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 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                636
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                                                                                                                                                                                                                                                                                                             691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      616 GluPheAspProProLysValTyrProProValProAla----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  596 ArgArgArgGluAspTrpProSerArgLeuGlnMetPhePheAlaAsnAsnHisAspGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATGGTCATTGCCATGAGCAGCATCGCCCTGGCCGCCGAGGACCCTGTGCAGCCCAACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgCysPheCysValGluCysValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                 sAspLeuGlyIleGlnValAspArgTyrIleAlaSerGluValCysGluAspSerIleTh 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrCysThrIleCysCysGlyGlyArgGluValLeuMetCysGlyAsnAsnAsnCysCys
                                                                                                                                                                                                                                                                                                                                                                   rValGlyMetValArgHisGlnGlyLysIleMetTyrValGlyAspValArgSerValTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AsnCysLysAsnCysPheLeuGluCysAlaTyrGlnTyrAspAspAspGlyTyrGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerCysGlySerLeuAsnValThrLeuGluHisProLeuPheValGlyGlyMetCysGln
                                                                                                                                                      GTGCTACGAC 4302
                                                                                                                                                                                   yLeuTyrGlu 725
                                                                                                                                                                                                                                              nAspLeuSerIle-----
                                                                                                                                                                                                                                                                              - CGACTTCATAGTGGTCAGTGGGGCCCT
                                                                                                                                                                                                                                                                                                    rGlnLysHisIleGlnGluTrpGlyProPheAspLeuValIleGlyGlySerProCysAs
                                                                                                                                                                                                                                                                                                                                        CCTGGGGCTCGTCCTGCATCAGGGT-----GCCTACTTCCGTGACCTCTGGAATATTCT 4192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgGluArgLeuValTyrGluValArgGlnLysCysArgAsnIleGluAspIleCysIle 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysProArgLysSerThrAlaGluLysProLysValLysGluIleIleAspGluArgThr
                                                                                                                                                                                                                  - TCACTGGCAATAGCAAAGGAAAAGACATCAACACGATTAAATCCCTCCGAGTCCTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------CCGTGGGGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGACGGCCCTAAGCCAATGCCTCCCTATAGCTCCATGTTCATCCTGTCCACGACCAA
                                                                                         Application US/08949386
                Harpold, Michae
Ellis, Steven
Williams, Mark
McCue, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ValLeuSerLeuPheAspGlyIleAlaThrGlyLeuLeuValLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GluLysArgLysProIleArg-----
                                              Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 08/14
FILING DATE: 5-NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 3,779
REFERENCE/DOCKET NUMBER: 519808
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/105,536 FILING DATE: 11-AUG-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
2813 GGACTTCCTCAG---GAAACAGGCCCGCTACCACGATCG---
                                                                 2753 CAACAAGAGCCGGGCCGAGCCCACCGTGGACCAGCGCCTCGGCCAGCAGCGCGCCGA
                                                                                                                               2696 GACGCACTTGGACCGGCCGCTGGTGGTGGACCCGCAGGAGAACCGCAA----CAACAACAC
                                                                                                                                                                                                   2636 AATGGACCCGGACGAGCGCTGGAAGGCTGCCTACACGCGGCACCTGCGGCCAGACATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 237..776
OTHER INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                               56
                                                                                             38 ArgGlnGluProSerThrThrAlaArgLys-----ValGlyArgProGlyArgLysArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                 22 Asp-----ArgLysAspGlyGluGluGluGluFroArgGlyLysGluGlu
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                             LysHisProProValGluSerGlyAspThrProLysAspProAlaValIleSerLysSer
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VENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS
VENTION: METHODS
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ጵ ຄ	76	ProSerMetAlaGlnAspSerGlyAlaSerGluLeuLeuProAsnGlyAsp 92
à	93	LeuGluLysArgSerGluProGlnProGluGlySerProAlaGl)
q	2918	
à	113	GlyalabroalagluGlyGluGlyAlaalaGluThrLeuProGluAlaSerArgAlaVal 132
ą	2969	GGGCAGCCTGGAGCAACCCGGGTTCTGGGAGGGCGAGGCCGAGGCG 3013
<u>ک</u> ځ	133	GluAsnGlyCysCysThrProLysGluGlyArgGlyAlaProAlaGlu 148
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≿ 8	149 3053	Aladiylysgiudinlysdiuthrash
ķ	158	IleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTrpGlu 177
ď	3113	
\$	178	SerSerLeuArgGlnArgProMetProArgLeuThrPheGlnAlaGlyAspProTyrTyr 197
ď	3173	GAGGGCGCGCACCGCGAGGGCAGCCGGC 3205
à	198	IleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLysLys
ą	3206	
À.	218	AlaLyBValIleAlaGlyMetAsnAlaValGluGluAsnGlnGly
e e	3260	
à	233	ProGlyGluSerGlnLysValGluGluAlaSerProProAlaValGlnGlnProThrAsp 25
g	3317	
ጵ	253	ProAlaSerProThrValAlaThrThrProGluProValGlySerAspAlaGlyAspLys 272
ą	3362	AACCAC 3388
à	273	AsnalaThrLysAlaGlyAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIle 292
g	3389	
3	293	GlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrpTrpPro 307
ရှ	3449	CATGAAGAACAACAGCTGGCCACCGGGGGAGTCGGCCGCTCCCCACGGCAGCCTTGGCCA 3508
à	308	GlyArgileValSerTrpTrpMetThrGlyArgSerArgAlaAlaGluGlyThrArgTrp 327
දි	3509	
ጵ	328	ValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLeu 347
q	3536	
ጵ	348	SerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLys 367
q	3545	
ጵ	368	AlaileTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPhePrc
q	3563	CCCTGC 3580
ጵ	388	HisAspSerAspGluSerAspThrAlaLysAlaValGluValGlnAsnLysProMetIle 407
વ	3581	CATGGCCACCACCCCCAGAACGCCGCCAGCCGGGACGCCCCAA 3625

y d	Oy 408 GluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGluP.	roProGluGlu	427
ò	Qy 428 GluLysAsnProTyrLysGluValTyrThrAspMetTrp	spMetTrp4	440
qq	3665 CCCCGAGAATAGCCTTATCGTCACCAACCC		3724
ò	441		455
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ò	Qy 456 LysProArgLysSerThrAlaGluLysProLysValLysGlullelleAspGluArs	Thr	475
g	3785 CCACACCGTCGTA	AGGA	3844
ò	Qy 476 ArgGluArgLeuValTyrGluValArgGlnLysCysArgAsnIl	eGluAspileCysile	495
Q	Db 3845 AGAGAAGAA	3	3853
ò	Qy 496 SerCysGlySerLeuAsnValThrLeuGluHisProLeuPheV	alGlyGlyMetCysGln 5	515
g	Db 3854		3859
ò	Oy 516 AsnCysLysAsnCysPheLeuGluCysAlaTyrGlnTyrAspAspAspGlyTyrGl	nSer	535
q	Db 3859	3	3859
δ	Qy 536 TyrCysThr1leCysClyGlyArgGluValLeuMetCysGl	удвпдвпдвпСувСув	ខ្លួ
рр	3860	E 3	3871
ò	Qy 556 ArgCysPheCysValGluCysValAspLeuLeuValGlyProGl	yAlaAlaGlnAlaAla	575
qq	Db 3871		3871
δ	576 IleLysGluAsp	rGlyLeuLeu	595
qa	Db 3872CCGTGGGGA		3880
ď	596 ArgArgA	apgln	615
Ωp	3881	ACCAA	3937
ò	616 GluPheAspProP	9	628
qq	3938 CCCCTTCGCCGCCTGTGCCATTACATCCTGAACCTGCG	CTACTTTGAGATGTGCATCCT 3	3997
ò	Oy 629		635
qq	3998 CATGGTCA		4057
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QQ	4116		4138
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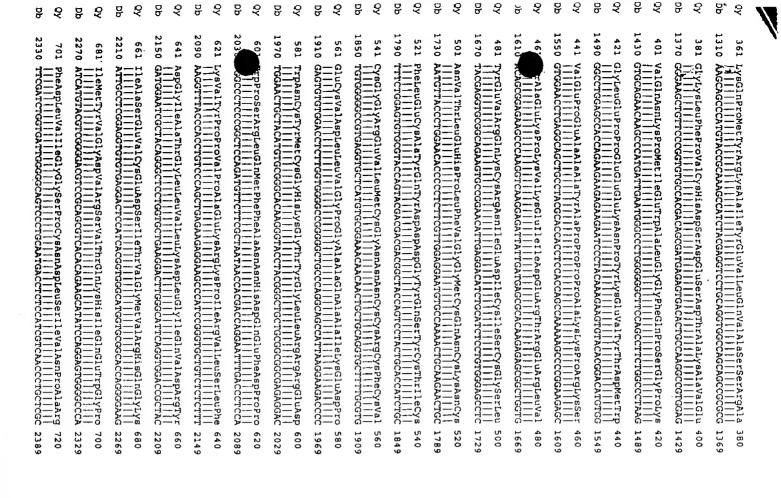
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COMMENT
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AUTHORS
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gene family
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complete cds.
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Direct Submission
Submitted (25-MAY-1998) CVRC, Parter, Charlestown, MA 02129, 3 (bases 1 to 3005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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ValGluLysLeuMetProLeuSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsn
                                                                                AlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLysPheSerValValCys
                                                                                                                                                                          ArgGlyPheSerTrpTrpProGlyArgIleValSerTrpTrpMetThrGlyArgSerArg
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חהכרינו	CTCTTCGCTCCGCTGAAGGAGTAT	LeuPheAlaProLeuLysGluTyrPheAlaCysVal	AGCCGCTTGGCGAGGCAGAGACTG	SerArgLeuAlaArgGlnArgLeuLeuGlyArgSerTrpSerValProValIleArgHis	TGCACTGAAATGGAAAGGGTATTT	CysThrGluMetGluArgValPheGlyPheProValHisTyrThrAspValSerAscMec	AAGCAGGGCAAAGACCAGCATTTT	LysGlnGlyLysAspGlnHisPheProValPheMetAsnGluLysGluAsp:leLeuTrp	CATGGCAGGATAGCCAAGTTCAGC	HisGlyArgIleAlaLysPheSerLysValArgThrIleThrThrArgSerAsnSerlle	ATGAACAGGCCGTTGGCATCCACT	MetAsnArgProLeuAlaSerThrValAsnAspLysLeuGluLeuGlnGluCysLeuGlu	GATGCCAAAGAAGTGTCAGCTGCA	AspAlaLysGluValSerAlaAlaHisArgAlaArgTyrPheTrpGlyAsnLeuProGly	ATGGGCGTTAGTGACAAGAGGGAC	MetGlyValSerAspLysArgAspIleSerArgPheLeuGluSerAsnProValMetIle	GCGCGGCCCAAGGAGGGAGATGAT	AlaArgProLy6GluGlyAspAspArgProPheFheTrpLouPheGluAsnValValAla	AAGGGCCTCTACGAGGGCACTGGC	LysGlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrArgLeubeuHsAsp
42° bp	Triccererere	PheAlaCysVal	CTGGGCCGGTCA:	LeuGlyArgSer	GGTTTCCCAGTC	GlyPheProValk	CCTGTCTTCATG	ProValPheMetA	AAAGTGAGGACCA	LysValArgThr]	GTGAATGATAAGG	ValAsnAspLysI 	CACAGGGCCCGCT	HisArgAlaArgT 	ATCTCGCGATTTC	leSerArgPheL	ceccerterie	ArgProPhePheT	CGCTCTTCTTTC	ArgLeuPhePheC
TRNA	2965	912	GGAGCGT	[rpSerVa	ACTATAC	lisTyrTh	ATGAGAA	\snGluLy	ATTACTAC	leThrTh	TGGAGCT	euGluLe 	ACTTOTO	yrPheΓη	rccacto	euGluSe 	GGCTCTT	 	AGTTCTA	luPheTy:
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Sequence 47, Application US/09276531

Patent No. 6183968

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.

APPLICANT: Yue, Henry

ICANT: Reddy, Roopa

ICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING

TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

COINTEN TO ALTO

STATE: CALIFORNIA
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US-09-276-531-47
COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.;

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/276,531

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/079,677

FILING DATE: March 27, 1998

CLASSIFICATION;

ATTORNEY/AGENT INFORMATION:
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4 US-09-152-060-36

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4 US-09-362-336A-1

4 US-09-362-336A-3

1 US-09-307-621-1

4 US-09-954-358-16

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4 US-09-962-284-3

1 US-08-804-227C-1

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5 US-08-804-227C-1

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NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2077 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TESTTUT02
CLONE: 1271435
US-09-276-531-47
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                  AspTyrPheAlaCysGlu
                                                                          LysLeuLeuGlyArgSerTrpSerValProValIleArgHisLeuPheAlaProLeuLys
                                                                                                               NTCTTTGGCTTTCCTGTGCACTACACAGACGTGTCCAACATGGGCCGTGGTGCCCGCCAG
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                                                         AAGCTGCTGGGAAGGTCCTGGAGCGTGCCTGTCATCCGACACCTCTTCGCCCCCTCTGAAG
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RESULT 2 US-08-913-832A-1



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Result
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Maximum DB
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-Q=/cgn2_1/USPTO_spool/US09720086/runat_18112002_092957_29457/app_query.fasta_1.4252
-Q=/cgn2_1/USPTO_spool/US09720086/runat_18112002_092957_29457/app_query.fasta_1.4252
-DB=Issuede_Patents_NA._OFMT=fastap_-SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-DDEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEASIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09720086_@CGN 1 1 108 @runat_18112002 _092957_29457 .NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXI=0.5 -FGAPOP=6 -FGAPEXI=7
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/FCTUS_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-913-159-12

US-08-960-745-4

US-08-960-745-4

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US-08-931-999-4

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US-08-951-742-7
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ALIGNMENTS

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/276,531

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
NUMBER OF SEQUENCES: 134 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 60/079, FILING DATE: March 27, 1998 CLASSIFICATION: STREET: 3174 PORT: CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: 94304 3174 PORTER DRIVE USA Lal, Preeti Hillman, Jennifer L. Bandman, Henry Roopa 01ga 60/079,677

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61 AGG---CGGCTCTTCTTCGAATTTTC-CACCTGAATTACTCACGCCCCAAGGAGGT 116
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Matches:
Conservative:
Mismatches:
Indels:
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NAME: Lynn B. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REGISTRATION NUMBER: 42,918
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 855-0556
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2077 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: 100PCLGY: linear
IMMEDIATE: SOURCE:
LIBRARY: TESTITUTO2
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87,86%
83,98%
18,78%
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Best Local Similarity:
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APPLICANT: Seelig, Hans Peter
TITLE OF INVENTION: DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
FILE REFERENCE: 8484-0030-999
CURRENT APPLICATION NUMBER: US/08/913,832A
CURRENT APPLICATION NUMBER: US/08/913,832A
CURRENT FILING DATE: 1998-01-12
PRIOR PILING DATE: 1996-03-08
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 6328
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Sequence 1, Application US/08913832A
Patent No. 6329517
GENERAL INFORMATION:
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33.90%
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; LOCATION: (1)...(5736)
US-08-913-832A-1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 6328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo : FEATURE: NAME/KEY: CDS LOCATION: (1)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/249,181A CURRENT FILING DATE: 1999-02-12 PRIOR APPLICATION NUMBER: US 08/913,832 PRIOR FILING DATE: 1998-01-12 PRIOR APPLICATION NUMBER: PCT/DE96/00444 PRIOR FILING DATE: 1996-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Seelig, Hans Peter
APPLICANT: Renz, Manfred
TITLE OF INVENTION: DERMATOMYOSITIS-SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 8484-0059-999
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                                                                                                                                                                                                                                                                         190 AAAATCCCTAAGÁGCAAGCGCCAAÁAAAAGGÁGCGTATGCTCTTÁTGCCGGCAGCTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                            88 CCACCCCACCCAGAAAATGAAGAGGACCCAGAAGAGGATTTGTCAGAA-----ACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AsnGluGluGluGlyAlaSerGlyTyrGluGluCysIleIleValAsnGlyAsnPheSer
                     uArgGlnArgAlaSerProArgIleThrArgGlyArgGlnGlyArgHisHisValGlnGl 151
                                                                                                                                                                                                                                                                                                                                                                                                                                           AspGlnSerSerAspThrLysAspAlaProSerProProValLeuGluAlaIleCysThr
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GAGAAGAAGAGCAAAT----
                                                                                                                                                           AspGlyAsnGlySerAsp-ileLeuMetProLysLeuThrArgGluThrLysAspThrAr
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                                                                                                gThrArgSerGluSerProAlaValArgThrArgHisSerAsnGlyThrSerSerLeuGl 131
                                                                                                                                                                                                                                      AspMetThrGlyAspGly-----AspArgAspAspGluVal------Asp
                                                                                                                                 GACAGTGAGGGCAGCGACTATACTCCTGGCAAGAAGAAGAAGAAGAAGCTTGGACCTAAG
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Matches:
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ò :		uTyrProValGluPheProAlaThrArgSerArgArgArgArgArgAlaSerSerSerAlaSe 171
ΩΩ		
ò	171 rT	rThrProTrpSerSerProAlaSerValAspPheMetGluGluValThrProLysSerVa 191 ;;;
qq	416	ATGATGATGATGATCAAAG-GAGCCTAAATCA 450
ò	191 lSe	SerThrProSerValAspLeuSerGlnAspGlyAspGluGluGlyMetAspThrThrGl 211
d G	451	tractcagcicctgaadactgggggaagagaagagacattgacca 494
ò	211 nVa	NValAspAlaGluSerArgAspGlyAspSerThrGluTyrGlnAspAspLysGluPheGl 231
Sp.	495 CGT	TGTTCTCAGAGGAGGATTATCGAACCCTCACCAACTAC
ó	231 yIl	ylleGlyAspLeuValTrpGlyLysIleLysGlyPheSerTrpTrpProAlaMetValVa 251
Db	535	
ò	251 lSe	SerTrpLysAlaThrSerLygArgGinAlaMetProGlyMetArgTr 267
QQ	567 TGC	cigccadadarcccaagatigcigictccaagatgatgatgatggtittgggigcaadatg 626
ò	267 pVa	alGlnTrpPheGlyAspGlyLysPheSerGluIleSerAlaAs 282
gg	627 GCG	GCGGGAGTTCAGTACTCCCTTCAAAGGCAGTTCTGGGGGCATCAGTGGCAGCTGC 686
ò	282 pLy	pLysLeuValalaLeuGlyLeuPheSerGlnHisPheAsnLeuAlaThrPheAsnLysLe 302
g	687 GGC	CAGCAGCAGCGGTAGCTGTGGAGAGCATGGTGAGCACTGAGGT 737
6	302 uVa	alSerTyrArgLysAlaMetTyrHisThrLeuGluLysAlaArgValArgAlaGlyLy 322
g	738 TGC	: TGCACCACCTCCCCCTGTGGAGGTGCCTATCCGCAAGGCCAAGACCAAGGAGGGAA 197
ò	322 BTh	#ThrPheSerSerSerProGlyGluSerLeuGluAspGlnLeuLysProMetLeuGluTr 342
qq	798 A	GGTCCCAATGCTCGGAGGAGGCCAGCCCTCGTGTACCTGA 845
ò	342 pAl	pAlaHisGlyGlyPheLysProThrGlyIleGluGlyLeuLysProAsnLysLysGlnPr 362
q	846 TGC	
ò	362 oVa	OVALVALABDLYSSerLySValArgSerAspSerArgAsDLe 377
q	879 CCT	:: CTGAAAATCAAGGTTTTGGTTCCAAGCGTAAGAGATCCTCGAGTGAGGAT 936
ò	377 uGl	uGluProArgArgGluAsnLysSerArgArgArgThrThrAsnAspSerAlaAlaSe 397
e G	937	GATGACTTAGATGTGGAATCTGACTTCGATGATGCCAGT 975
ò	397 rGl	rGluSerProProProLysArgLeuLysThrAsnSerTyrGlyGlyLysAspArgGlyGl 417
a	9/6	
à	417 uAs	spGluGluSerArgGluArgMetAlaSerGluValThrAsnAsnLysGlyAsnLeuGl 437
qq	1008 CAG	CAGCCGTAGTAGCCGCAGCCGCAAGAAACTCCGAACCACTAAAAAGAAAAAAAA
ć	437 uAs	uAspArgCysLeuSerCysGlyLysLysAsnProValSerPheHisProLeuPheGluGl 457
g	1068 GGA	GGAGGAGGTGACTGCTGTG 1086
ત્રે	457 yGl	yGlyLeuCysGlnSerCysArgAspArgPheLeuGluLeuPheTyrMetTyrAspGluAs 477
g	1087	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
À.	477	pGlyTyrGlnSerTyrCysThrValCysCysGluGlyArgGluLeuLe 493
දි	1089 TGG	GTTATGAGACAGACCAGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCAT 1148

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/strandard_name= "Gene coding for R.LlaDII"
/label= r-llaDII
/note= "The first ten amino acids in this sequence may be doubtful. However, from base 773 this reading frame gives a homology with the Bsp61 endonuclease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFFLICANT OF INVENTION: Plasmid-derived type II
TITLE OF INVENTION: restriction-modification systems from Lactococcus lactis
NUMBER OF SEQUENCES: 14
NUMBER OF SEQUENCES: 14
NUMBER OF SEQUENCES: 14
NUMBER OF SEQUENCES: 14
NEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENCIEN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,159
                           1195 ------CCCGACATGGAGAGGCTCCCGAGGCAAGTGGAGCTGCCCACACTG 1241
                                                                                                                                                                                                                                                       1242 CGAGAAGGAA-----GGCATCCAGTGGGAAGCTAAAGAGGACAATTCGGAGGTGA 1292
                                                                                              513 lGlyAlaGlyThrAlaGluAspAlaLysLeuGlnGlu---ProTrpSerCysTyrMetCy 532
493 uLeuCysSerAsnThrSerCysCysArgCysPheCysValGluCysLeuGluValLeuVa 513
                                                                                                                                                                                                     532 sLeuProGlnArgCysHisGlyValLeuArgArgArgLysAspTrpAsnMetArgLeuGl 552
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LOCATION BETHOD: experimental
OTHER INFORMATION: /codon.start= 1392
OTHER INFORMATION: /codonce= "Liabli methylase"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ORF"
OTHER INFORMATION: /fumber= "OTHER INFORMATION: /fumber= "Gene coding for M.Llabli"
OTHER INFORMATION: /label= m-llabli
OTHER INFORMATION: /label= m-llabli
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FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRILING DATE: 17-FEB-1995
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2355 base pairs
TYPE: nucleic acid
STRANDEDRESS: double
TYPE: DAY (genomic)
HYPOTHETICAL: NO
ANTI-SENSE:: NO
ONIGINAL SCURCE:
ORIGINAL SCURCE:
ORGANISM: Lactococcus lactis subsp. cremoris
FRAIN: W39
FRATUDE:
                                                                                                                                                                                                                                                                                                                                                         1293 GGAGATCCTGGAAGAGTTGGGGGAGACCTCGAAGAG 1329
                                                                                                                                                                                                                                                                                                       552 nAspPhePhe---ThrThrAspProAspLeuGluGlu 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08913159; Patent No. 6300109; GENERAL INFORMATION:
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LOCATION: 744..1283
IDENTIFICATION METHOD:
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                                  796
                                                                                                       784
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                                                                                                                                         AATATGACTAATCACGACACTACATATCAGTGGCGTAGAGTTTATGTAAGAGAAAACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAGCTGATGAAATACCAGATTTTGATATTATGTTAGCAGGTTTTTCCTTGCCAAGCCTTT 1616
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                                                                                                                                                                                                                                                                                                                                                        AATAGAGAACGTATCTATATTGTTGCTTTCAAAAATAAAAAGATTATGCAAATTTTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTGAACTTGTTCGTATTTTAGAAACAAAAAAACCTCGTGTTGCA------
                              ProValValMetAsnGlyLysAspAspValLeuTrpCysThrGluLeuGlu-----Arg
CCTATAATCCTTACATATAGCGGAGATATTCGTAAATTAACACCAAGAGAATGCTTTAAC 2210
                                                                   AGTAATTTAGTACCAACACTAACGGCTAATATGGGAACAGGTGGGCATAAT-----GTG 2150
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156.00
35.48%
22.87%
3.40%
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    ThrAlaLysLeuLysLysValGlnThrIleThrThrLys 783

                                                                                                                                                                                                                                                                                                                  -LysLeuGluLeuGlnAspCysLeuGluPheSerArg---
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Matches:
Conservative:
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                                                                                                   -ArgGlnGlyLysAsnGlnLeuPhe
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                                    Best Local Similarity:
Query Match:
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                                                                                                                                    ; CLONE: US-08-760-745-4
US-09-720-086-6 (1-859) x US-08-760-745-4 (1-2376)
                                                                 Percent Similarity
                                                                                                       Alignment Scores:
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                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM
MEDIUM TYPE: Disketi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Goli, Surya K.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: LUNG GROWTH
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                            No.:
                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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598956
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                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version
                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                              TELEPHONE: 415-855-0555
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                          Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
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142 GlyArgGlnGlyArgHisHisValGlnGluTyrProValGluPheProAlaThrArgSer 161

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GGGTGGAGGAAGAGGCCTCGCGCAGAGGAGCAATTGAATTTCAAACACAACAACAACAACAACAACAACAACAACA	ACGCCGCACAGCCAAACTTGGGCTCCCGCCCGGGGGGGGG		
25 162 182 139 202 222	N at 10 at 1- at 10 at 10	2 2 2 2 2 2 2 2	366 379 379 3179 3179 317 415 429 446 446
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1322 AGGTGGATGAACGAGCCCAAGCTGAGCTCGCCCAAGAGGTTTTTCAGGGAGATGG 1381
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                                                                                                                                                                                                                                          APPLICANT: Lina, Elizabeth J.
APPLICANT: Pestonjamasp, Kersi N.
APPLICANT: Pope, Robert K.
APPLICANT: Pope, Robert K.
APPLICANT: Mulfkuhle, Julia D.
TITLE OF INVENTION: ACTIN-BINDING POLYPEPTIDES
NUMBER OF INVENTION: AND NUCLEIC ACIDS ENCODING THE SAME
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
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Matches:
Conservative:
Mismatches:
Indels:
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COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/962,284
FILING DATE: 31-027-1997
ATTORNEY/AGENT INPORMATION:
NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/058001
TELEFONE: 617/542-5070
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                                                                                                                                                                    Sequence 1, Application US/08962284; Patent No. 5985608; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: Coding Sequence
) LOCATION: 451...5814
US-08-962-284-1
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144.50
32.24%
20.39%
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                    1108 CATGGCCTGCAAA 1120
460 sGlnSerCysArg 464
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Best Local Similarity:
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Pred. No.:
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US-08-962-284-1
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322 2386	304 erTyrArgLysAlaMetTyrHisThrLeuGluLysAlaArgValArgAlaGlyL	р 2
ũ	267 GGGACAGGCTGCCCTTTGAAGAGAAGGTGGAGGTGGAGAATGTTATGAAAAGGAAGTTTT	N
304	301LysLeuVals	Ş
300	288 lyLeuPheSerGlnHisPheAsnLeuAlaThrPheAsn	Qy Db 2
2206	147 AATATGCTGTTCCCAGAAGAGGAAGCCTGGAACGGGCGAACCCTCCCATCACCCACC	Db 2
288	LeuG	γQ
_ 0	087 CAGAAGCATCCTACCCCATCCTGAACAGAGCCAGGGAAAGGAGACAGCCATAAGGAATCTA	N
י פ	279]eSerA aAso	
279 2086	265 etArgTrpValGlnTrpPheGlyAspGlyLysPheSerGluI	망 2
2047	988 AGAACAAGGGAATGTTGAGAGAATATGGAGAGACAGAAAGCAAGAGAGCTTTGACAGGTC	Db 1
265	rSerLysArgGlnAlaMetProGlyM	δ
1987	948CTGAAATCGCAAGCTTGGCAGCCTTTGGTAGAGGGTAGCG	Db 1
247		ş
233 1947	216 erArgAspGlyAspSerThrGluTyrGlnAspAspLysGluPheGlyIleG	D 29
8	829 TTGCTCCAATGTATGCCGGAGATCTTCGCACAAAGCCACCTCTTGACCACAATGCAAGTG	μ
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00 1	796 TGAACACATCAGTGTCTACCGTAGCATCCACGG	1
196	SerThrProSerV	Ş
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158 1735	138 rgIleThrArgGlyArgGlnGlyArgHisHisValGlnGluTyrProValGlnPheProA	음 성
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ō,	633TTGTTTAACAAATTGTCCCAGCCAGTCTCAAAAG	
118	ProLysLeuThrArgGluThrLysAspThrArgThrArgSerGluSerProA	δ
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98	<pre>[hrGlyAspGlyAspArgAspAspGluValAspAspGlyAsnGlySerAspI</pre>	γQ
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608 IleAlaSerGluValCysAlaGluSerIleAlaValGlyThrValLysHisGluGly 626	γQ
3307 ACTGAGCAGAGATTAAACGTTGCCTTCATGGAGTCAAAGCGGATGAAAGTAGAAAAAGATG 3366	망
595LeuValLeuLysGluLeuGlyIleLysValGluLysTyr 607	Ş
3247 CAGGCCTCCAAAAACCCCCTGAAAATGCTGGCGGCAAGAAATCTCCTTCAGGAATAC 3306	B
LeuSer	Ş
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567 ProLysLeuTyrProAlaIleProAlaAlaLysArg578	Ş
CCAAGAAGTCCTGTGGAGGATGAAGGACTTCGATGTCATTTTCGATCCTTATGCA 31	망
550 ArgLeuGlnAspPhePheThrThrAspProAspLeuGluGluPheGluPro 566	Ş
541 DEMARG	B &
AAAGTTGGCGGGATGCACGAAACGGTGCTCACTGTCACCGGCAAATCTGTGAAGGAGGTG) B
roTrpSerCysTyrMetCysLeuProGlnArgCysHisGly-Val 5	Ş
2994AAGAAGGCTGAATAAC 3009	Db .
501 ysArgCysPheCysValGluCysLeuGluValLeuValGlyAlaGlyThrAlaGluAspA 521	γQ
2938 AGACCAGATATGCAGTTAGAATCGGACCTGAAGTTGGACAGGCTGGAAACCTTTCT 2993	Дb
482 yrCysThrValCysCysGluGlyArgGluLeuLeuLeuCysSerAsnThrSerCysC 501	γQ
2878 ATTTGCGGTAAAACAAGAGGCACCACACCCGTTTCCAAACCCCCTGGAAGATATCGAAGCC 2937	D D
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2829GAAGAAAGGTTTGGCGTCACCTACTGCCATAACCCCAGTAGCCTCAGCC 2877	망
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erTyrGlyGly	γQ
383 10ASDLYBSEFAIGAIGAIGAIGINFINIASIMSPSEFAIGAIGSEFGIUSEFFTOFFOF 402	B &
64 TEGCACTETTGAAGAAAAGCEGGGAAGAATTGGAGAAAACAGACTCAGCAGGAGGCAGG) B
alValAsnLysSerLysValArgArgSerAspSerArgAsnLeuGluProArgArgArgG 38	. Ş
2507 CGACAGGGGAGGGCCTTCTTGACTCACCCAGCAAAACCATGTCTATTAAAGAAAG	В
349 roThrGlyIleGlyLeuLysProAsnLysLysGlnProV 363	Ś
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lnLeuLysProMetLeuGluTrpAlaHisGlyGlyPheLysP 3	ફ.
322 ysThrPheSerSerSerProGlyGluSerLeuGluAspG 335	유 성

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3367 TCTTCCAACTCCAACTTCTGGAAAGTCACCCTGGGGGGTTTAGCCAGTAAAGAAAACTTC 3426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     679 PheGluPheTyrHisLeuLeuAsnTyrThrArgProLysGluGlyAspAsnArgProPhe 698
                                                                                                                                         627 ------GlnIleLysTyrValAsnAspValArgLysIleThrLysLysAsnIleGlu 643
                                                                                                                                                                                                                                                                                                                                        644 GluTrpGly---ProPheAsp------LeuValileGlyGlySerProCysAsn 658
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Patent No. 6043219
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                              COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,999
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Mismatches:
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Matches:
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Gaps:
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INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 6755 base_pairs
                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/710,561
FILING DATE: 19-SEP-1996
ATTORNEY/AGENT INFORMATION:
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STRAIN: UT0007
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Percent Similarity: 35.01%
Best Local Similarity: 19.90%
Query Match: 2.89%
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STRANDEDNESS: double
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U.S.A.
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COUNTRY:
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Patent No. 5616485
                                                                                                                    APPLICANT: Butler, Michael J.
APPLICANT: Hadary, Dany
APPLICANT: Jenish, David
APPLICANT: Krieger, Timothy
TITLE OF INVENTION: STREPTOMYCES PI
TITLE OF INVENTION: STREPTOMYCES STRIPTOMYCES STREPTOMYCES STREPTOMYCE
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                                                          NUMBER OF SEQUENCES:
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3000 K Street, N.W
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                        Foley & Lardner
                                                                ADDRESS
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                                                                                                                                                         PROTEASES AND IMPROVED STRAINS FOR EXPRESSION
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
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LENGTH: 1820 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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139 eThrArgGlyArgGlnGlyArgHisHisValGlnGluTyrProValGluPheProAlaTh : |||||||
                                               414 GCGACGTCCGGCTCGCGCTGGCCCGCAAGAAGGCCACGGGGCCCAGGCCAAGCGCCTCGGCT
                                                                                                                                                                                                                                                                                                    195 GCTCGGCCGG
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                 56 rArgGlyArgArgSerSerSerArgLeuSerLysArgGluValSerSerLeuLeuAsnTy
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Matches:
Conservative:
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QQ	474	CGCTGCTGGTCAACCCGGGCGGAC-CGGGCGCTCGGCGATCGGCTACCTCCAGCAGTAC 532
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ò	6	21
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q	673	ggacgácgggggggggggggggggggggggggggggggg
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දු ද	251	ISerTrpLysAlaThrSerLysArgGlnAlaMetProGlyMetArgTrpValGlnTrpPh 271
ò	271	eGlyAspGlyLysPheSerGluIleSerAlaAspLysLeuValAlaLeuGlyLeuPheSe 291
qq	814	::: :: GGGCGACGTTCCTGGGC 865
ò	291	rGlnHisPheAsnLeuAlaThrPheAsnLysLeuValSerTyrArgLys 307
QQ	998	GGACCTACGCCGGTCTGTTCCCCGACGGGCCGCCTGGT 909
ò	308	AlaMetTyrHisThrLeuGluLysAlaArgValArgAlaGlyLysThr 323
q	910	
ò	324	PheSerSerProGlyGluSerLeuGluAspGlnLeuLysProMetLeuGl 341
q	970	GGGCTTCGAGACGGCGTTCCAGTCCTTCGCGAAGGÁCTGCGTGÀÁGCAGCCÓGA-CTGCC 1028
à	341	uTrpAlaHisGlyGlyPheLysProThrGlyIleGluGlyLeuLysProAsnLysLysGl 361
q	1029	cctcgggacaaddacaccacccc
ð :	361	spSerArgAsnLeuGluProArgAr
g	1071	ACCTCAAGTCCTTCTTCGACGACCTGGACG 1100
<u>ک</u> ۾	381	gargGluasnLysSerArgargArgThrThrasnAspSerAlaaNaSerGluSerProPr 401
ò	401	oproLysArgLeuLysThrAsnSerTyrGlyGlyLysAspArgGlyGluAspGluGluSe 421
q	1160	
ò	421	rArgGluArgMetAlaSerGluValThrAsnAsnLysGlyAsnLeuGluAspArgCysLe 441
q	1207	GCGCGAGTCCCTCACCTCGCCGATCAAGGAGGACGGT
ò	441	uSerCysGlyLysLysAsnProValSerPheHisProLeuPheGluGlyGlyLeuCysGl 461
q	1247	GCGGGCCTGCT 1263
à	461	nSerCysArgAspArgPheLeuGluLeuPheTyrMetTyrAspGluAspGlyTyrGlnSe 481
Q	1264	
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q	1298	

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APPLICANT: Bartfeld, Daniel
APPLICANT: Bartfeld, Daniel
APPLICANT: Butler, Michael J.
APPLICANT: Haddary, Dany
APPLICANT: Haddary, Dany
APPLICANT: Haddary, David
APPLICANT: Krieger, Timothy
APPLICANT: Malek, Lawrence T.
APPLICANT: Marking ENTERPTOMYCES PROTEASES AND IMPROVED
TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES
NUMBER OF SEQUENCES: 21
CORRESPONDENCES: 21
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CONTRESPONDENCES 31
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                                                     1354 CGCCTTCTCCTCCCGGACGAGGTGCGCGACGCCCTCCCCGACTTCGAGAAGGCGTCCCC 1413
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501 sArgCysPheCysValGluCysLeuGluValLeuValGlyAlaGlyThrAlaGluAspAl 521
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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FILING DATE: 24-JUN-1994
CLASSIPICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US 08/173,508
FILING DATE: 13-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAMME: BENT, SCEPHEN A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08265310; Patent No. 5856166; GENERAL INFORMATION:
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TELEFAX: 202 672 5399
TELES: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
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216 rArgAspGlyAspSerThrGluTyrGlnAspAsp-----LysGluPheGlyIleGly-- 233
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                                CCCGTCGAGTGCCTG-GACGGGCGCGAGATGGACGCGTACACGCGCACCGACGTCACCCC 672
                                                             pLeuSerGlnAspGlyAspGlnGluGlyMetAspThr---ThrGlnValAspAlaGluSe 216
                                                                                                                          oAlaSerValAspPheMetGluGluValThrProLysSerValSerThrProSerValAs 197
                                                                                                                                                                                      rArgSerArgArgArgAlaSerSerSerAlaSerThrProTrp-----SerSerPr 177
                                                                                                                                                                                                                      CGCTGCTGGTCAACCCGGGCGGAC-CGGGCGGCTCGGCGATCGGCTACCTCCAGCAGTAC
                                                                                                                                                         GCGGGCATCGGCTACCCGGCGAAGGTCCGCGCCCAGTACGACATGGTGGCGGTCGACCCC 592
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Q	Дb	Q Q	Db	S S	B &	Db	Qy	Дb	8	Db	Оy	Db	Qy	Db	99	Db	99	Db	ργ	Db	ργ	Дb	Q	дb	γΩ	Db	8	da	Ş	Db	γQ	Db	9	Db
559 oAspLeuGluGluProProLysLeuTyrProAlaIleProAlaAlaLysArgAr 579		539 yValleuArgArgArgLysAspTrpAsnMetArgLeuGlnAspPhePheThrThrAspPr 559		521 aLysLeuGlnGluProTrpSerCysTyrMetCysLeuProGlnArgCysHisGl 539	501 sArgCysPheCysValGluCysLeuGluValLeuValGlyAlaGlyThrAlaGluAspAl 521	1298	481 rTyrCysThrValCysCysGluGlyArgGluLeuLeuLeuCysSerAsnThrSerCysCy 501	1264 CTCCGACAGCTACTACGAGCGCGAGGCCGACGGC 1297	461 nSerCysArgAspArgPheLeuGluLeuPheTyrMetTyrAspGluAspGlyTyrGlnSe 481	1247GCGGGCCTGCTGATCCT 1263	441 uSerCysGlyLysLysAsnProValSerPheHisProLeuPheGluGlyGlyLeuCysGl 461	1207 GCGCGAGTCCCTCGGCGATCAAGGAGAAGGACGGT 1246	421 rArgGluArgMetAlaSerGluValThrAsnAsnLysGlyAsnLeuGluAspArgCysLe 441	1160 ACCGGCGTG-ATCGCCGCGATGTACGACGAGGGCGCCTGGCAGCAGCT 1206	SerTyrGlyGly	1101 CGAAGCCCCTGCCGGCGGACGCCG-ACGGCCGCAAGCTCACCGAATCCCTCGCCACC 1159	381 gArgGluAsnLysSerArgArgArgThrThrAsnAspSerAlaAlaSerGluSerProPr 401	1071 ACCTCAAGTCCTTCTTCGACGACCTCGACG 1100	AsnLysSe	CCCTCGGCGACAAGGACACCACCCCCGACCAGGTCGGCAAGA	341 uTrpAlaHisGlyGlyPheLysProThrGlyIleGluGlyLeuLysProAsnLysLysGl 361	970 GGGCTTCGAGACCGCGTTCCAGTCCTTCGCGAAGGACTGCGTGAAGCAGCCGGA-CTGCC 1028	324PheSerSerSerProGlyGluSerLeuGluAspGlnLeuLysProMetLeuGl 341	910 CCTGGACGGCGCGGATGGACCCCTCGCTGCCCGCCGCCCTGGAACCTGGAGCAGACGGA 969	308AlaMetTyrHisThrLeuGluLysAlaArgValArgAlaGlyLysThr 323	ессесств	rGlnHisPheAsnLeuAlaThrPheAsnLysLeuValSerTyrArgLys	814 GGGCGACGAGGACCTACGTGGGAGCGTACGGCACCTTCCTGGGC 865	271 eGlyAspGlyLysPheSerGluIleSerAlaAspLysLeuValAlaLeuGlyLeuPheSe 291	760 CCACGTCTCCACGGTCGAGGCGGCACGCGGACGTGGACGTCCTGCGCGGGGGGGCT 813	251 lSerTrpLysAlaThrSerLysArgGlnAlaMetProGlyMetArgTrpValGlnTrpPh 271	733 CGGGGCGGACGCG	234AspLeuValTrpGlyLysIleLysGlyPheSerTrpTrpProAlaMetValVa 251	

DD 1474		
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	rLeuPheAspGlyIleAlaThrGlyTyrLeuValLeuLysGluLeuGlyIleLysValGl :	
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RESULT 10 US-08-951-74 Sequence 7 Parent No. GENERAL I APPLICA APPLIC		
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195 GCTCGGCCGG------GGGCGCGTCGACGTCCCCCGGGGCGAGGCGG 245
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                                                                                                  uLysTyrIleAlaSerGluValCysAlaGluSer------IleAlaValGl
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                                                                  CGCGTACGGCCGCCAGCTCCTGCATCGACTCCGCGATCAACACGTACCTGCTGACCGG
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                               YThrValLysHisGluGlyGln 627
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Best Local Similarity:
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DB:
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Patent No. 5985283
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APPLICANT: HATEBO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
NAME: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,679
FILING DATE: 12-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 62
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ADENOVIRUS TITLE OF INVENTION: INHIBITOR (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                 301
                                                                                                                                                                                                          254 LysAlaThrSerLysArgGlnAlaMetProGlyMetArgTrpValGlnTrpPheGlyAsp
                                                                                                                                                                                                                                                                          234 AspLeuValTrpGlyLysIleLysGlyPheSerTrpTrpProAlaMetValValSerTrp
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LOCATION:
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
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1152 GCAGAATCCAGTATCTCCTCCACCAGTAATGAGCAGCTAAAGGTCACTCAAGAACCAAGA 1211
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1032 CTGCACGTGAAGCGCAGTATGGGTTGGAAAAAGGCCTGTGATGAGCTGGAGCTGCATCAG 1091
                                                                                          1092 CGTTTCCTACGAGAAGGGAGATTTTGGAAATCTAAGAATGAGGACCGAGGTGAGGAAGAG 1151
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                                              316 AlaArgValArgAlaGlyLys----- 322
                                                                                                                                           323 -----ThrPheSerSerSerProGlyGluSerLeuGluAspGlnLeuLysProMet 339
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NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
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COUNTRY: US
ZIP: 53701-2113
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31583 ATAGAAACTAATAAGAGACGTTGCAACTATATGAATGTAATAGAATTGTTTTTCTGGCGTT 31524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             704 AsnValValAlaMetLysValAsnAspLysLysAspIleSerArgPheLeuAlaCysAsn 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----MetileAspAlaileLysvalSerAlaAlaHis---- 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           573 IleProAlaAlaLysArgArg-----ProlleArgValLeuSerLeuPheAspGlylle 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   611 GluValCysAlaGluSerIleAlaValGlyThrValLysHisGluGlyGlnIleLysTyr 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          631 ValAsnAspVal------ArgLysIleThrLysLysAsnIleGluGluTrpGly 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     664 AshProAlaArgLysGlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrHis 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuLeuAsnTyrThrArgProLysGluGlyAspAsnArgProPhePheTrpMetPheGlu 703
           COMPUTER: Diskette, 3.50 inch. 1.44Mb storage COMPUTER: Diskette, 3.50 inch. 1.44Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/453,702B FILING DATE: 03-Dec-1999 CLASSIFICATION CURROWN-PRIOR APPLICATION NUMBER: 60/110,955 FILING DATE: 04-DEC-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-720-086-6 (1-859) x US-09-453-702B-96 (1-34063)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE; DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 96:
08-09-453-702B-96
                                                                                                                                                                                                                                                                                NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (608) 251-9
INFORMATION FOR SEQ ID NO: 96.
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
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40.69%
25.11%
2.73%
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JLE TYPE: DNA (s
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 34063
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Best Local Similarity:
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DB:
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Percent Similarity:
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TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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                                                                                                                                                        Db 1606102 CTGCCGCTGGATGGCACCGGCGGTGCTCCGCGCCAAACAATAGTGTCTCGGTAACCGCCG 1606161
                                                                                                                                                                                                                                              Db 1606042 ATGCGGACAGAATCTCGACGATCCCGATGCCGCTTTCGGGTTGCAGATGGCGCTGGAGGT 1606101
                                                                                                                                                                                                                                                                                                                                         Db 1606027 CCAGGCGATGGAACT------
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                                                                      Db 1606162 GTCCGTTCATGCCGTGCGCAC-----
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: WHITE, OWEN R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31088 GCTCCAACTATTCGAACTAGATATTTTTTTT-----
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162 ArgArgArgAlaSerSerSerAlaSerThrProTrpSerSerProAlaSerValAsp 181
                                                                                                                                                                                           125 -----AsnGlyThrSerSerLeuGluArgGlnArgAlaSerProArgIleThrArg 141
                                                                                                                                                                                                                                                                                       112 ThrArqSerGluSerProAlaValArqThrArqHisSer------
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                                                                                                             142 GlyArgGlnGlyArgHisHisValGlnGluTyrProValGluPheProAlaThrArgSer 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ence 1, Application US/09103840A
nt No. 6294328
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                                                                                                                                                                                                                                                                                                                                                                       92 AspGlyAsnGlySerAspIleLeuMetProLysLeuThrArgGluThrLysAspThrArg 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 MetThrGlyAspGlyAspArgAspAspGluVal----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 ArgSerSerSerArgLeuSerLysArgGluValSerSerLeuLeuAsnTyrThrGlnAsp 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-086-6 (1-859) x US-09-103-840A-1 (1-4411529)
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125.50
30.39%
21.85%
2.73%
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Matches:
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36
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                                                                  ----AATCGTGGT 1606191
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Db 1607145 CCTGACGTTCAACGGTGCGACCCCGGACCACCGACTACGCGACCAC
1607100GGGCATCCTCGCCCGGTTTCCGGGTCTGTACCTGCAGTCGCTCG
y 439 ArgCysLeuSerCysGlyLysLysAsnProValSerPheHisProLeuPheGluGly 457
Oy 419 GluGluSerArgGluArgMetAlaSerGluValThrAsnAsnLysGlyAsnLeuGluAsp 438
Qy 402ProLysArgLeuLysThrAsnSerTyrGlyGlyLysAspArgGlyGluAsp 418
Qy 394 SerAlaAlaSerGluSerProPro
Qy 376 AsnLeuGluProArgArgArgGluAsnLysSerArgArgArgThrThrAsnAsp 393
Qy 366
36 36
Qy 339 MetLeuGluTrpAlaHisGlyGlyPheLysProThrGlyIleGlu 353
Qy 319 ArgAlaGlyLysThrPheSerSerProGlyGluSerLeuGluAspGlnLeuLysPro 338
Qy 299 PheAsnLysLeuValSerTyrArgLysAlaMetTyrHisThrLeuGluLysAlaArgVal 318
Qy 288 GlyLeuPheSerGlnHisPheAsnLeuAlaThr
Qy 270TrpPheGlyAspGlyLysPheSerGluIleSerAlaAspLysLeuValAlaLeu 287
Qy 253 TrpLysAlaThrSerLysArgGlnAlaMetProGlyMetArgTrpValGln 269
Oy 241LysGlyPheSerTrpTrpProAlaMetValValSer 252
Qy 222 ThrGluTyrGlnAspAspLysGluPheGlyIleGlyAspLeuValTrpGlyLysIle 240 It is a control to the control of the
Oy 202 GlyAspGlnGluGlyMetAspThrThrGlnValAspAlaGluSerArgAspGlyAspSer 221
Qy 182 PheMetGluGluValThrProLysSerValSerThrProSerValAspLeuSerGlnAsp 201
Db 1606192 CGTGAGCTTCGGTGTCGGCGCATATGGTCTCCGACGGATTCGGCGCCT 1606239

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Db 1607533 CCGGTGCACCATCGACCCGATCGCAGTCGCCCCAGATAGGCGCTGCGATCGGTGGTCG 1607592
                                                   Db 1607190 CATTTACACGACCCAATACGACGCTTTGCCGACTTCCCGAAGTACCCGCTCAACATCCT 1607249
                                                                                                                                                           Db 1607250 GGCGGACGTCAACGCGCTGCTGGGTATTTACTATTCGC-ACAGCTTGTATTACGGGCTCA 1607308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 1607447 TCATCGAGCCAGACCAGC-----1607488
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                                                                                                                                                                                                                                                                          552 GlnAspPhePheThrThrAspProAspLeuGluGluPheGluPro---ProLysLeuTyr 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                571 Pro-----AlaAlaLygArgArgPro 580
                                                                                                        476 ------GluAspGlyTyrGlnSerTyrCysThrValCysCuGluGly--- 489
                                                                                                                                                                                                                           512 LeuValGlyAlaGlyThrAlaGluAspAlaLysLeuGlnGluProTrpSerCysTyrMet 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 CysLeuProGlnArgCysHisGlyValLeuArgArgArgLysAspTrpAsnMetArgLeu 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         581 IleArgValLeuSerLeuPheAspGly----- 589
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SOFTWAREN PAPPLICATION DATA:
APPLICATION NUMBER: US/09/254,325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ENHANCED EXPRESSION OF TITLE OF INVENTION: PROTEOLYTIC ENZYMES IN KOJI MOLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oy 607 TyrileAlaSerGluValCysAlaGluSerileAlaValGly 620
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6090607
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SEQUENCE CHARACTERISTICS:
LENGTH: 4657 base pairs
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TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION: 1189..1604
FEATURE:
472 TyrMetTyrAsp---
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US-09-254-325-1
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2398 ACGGATTICTICTCCACCGCCATCAGGCTACCAGGCCACCGCCATCC----- 2445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2617 TCGACGGTGCATTCGCCGAGCTACCCCATTCCCCAGCCGCAACATGTGGACCCCACTCAG 2676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2677 GTGTTGAACGCCACCAATTACTCGACCGGCAACTCCCACCATACCGGCGCCATGTTTTCA 2736
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ZIP: 101
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STATE: NY
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5643 base pair
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TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM CON
OPERATING SYSTEM:
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STRAIN: IFO4177
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IBM Compatible
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Search completed: November 25, 2002, 02:56:29 Job time : 4354.34 secs

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Sequence 47, Application US/09276531
Patent No. 6183968
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Hilfman, Jennifer L.
PPLICANT: Yue, Henry
                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6...
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/276.531
FILING DATE: Herewith
CLASSTEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-09-276-531-47
         CLASSIFICATION: DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/079,
PILING DATE: March 27, 1998
CLASSIFICATION:
                                                                                                                                                                                                          APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCORE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
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US-08-800-644-9
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US-08-8149-097D-22
US-08-149-097D-22
US-08-149-097D-22
US-09-135-008-6
US-09-535-008-7
US-09-105-537-5
US-09-105-537-5
US-09-105-537-5
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US-09-720-086-7 (1-912) x US-09-276-531-47 (1-2077)
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DB:
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Best Local Similarity:
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TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2077 base pairs
TYPE: nucleic acid
STEANDENNES
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REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
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TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TESTTUT02
CLONE: 1271435
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                                                                    ArgLeuLeuGlyArgSerTrpSerValProValIleArgHisLeuPheAlaProLeuLys
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AF068625
Mus musculus DNA cycosine-5 methyltransferase 3A (Dnmt3a) mRNA,
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Okano, M., Xie, S. and Li, E.
Cloning and characterization of a family of novel mammalian
(Cytosine-5) methyltransferases
(Cytosine-5, methyltransferases
Nat. Genet. 19 (3), 219-220 (1998)
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Direct Submission
Submitted (28-MAY-1998) CVRC,
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On Nov 18, 1999 this sequence version replaced gi:3327977
Location/Qualifiers
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Submitted (04-NOV-1999) CVRC, Mass. Gen. Hospital,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (bases 1 to 4192)
Okano, M., Chijiwa, T., Sasaki, H. and Li, E.
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/pro
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                                                                                                                                                    QJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to EST sequences deposited in GenBank
Accession Numbers AA052791, AA111043, AA154890, AA240794,
AA756653, W58898, W59299, W91664, and W91665"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
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/function="de novo DNA methylation"
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Sciurognathi; Muridae; Murinae; Mus
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	700 2316	681 GlyAspValArgSerValThrGlnLysHisIleGlnGluTrpGlyProPheAspLeuVal	
	680 2256	661 ValCysGluAspSerIleThrValGlyMetValArgHisGlnGlyLysIleMetTyrVal	
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•	640 2136	621 ProValProAlaGluLysArgLysProIleArgValLeuSerLeuPheAspGlyIleAla	
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	\$80 1956	LeuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTrpAsnCysTyr	
	560 1896	41 GluvalLeuMetCysGlyAsnAsnAsnCysCysAr 	
	540 1836	521 AlaTyrGlnTyrAspAspAspGlyTyrGlnSerTyrCysThrIleCysCysGlyGlyArg	
	520 1776	01 GluHisProLeuPheIleGlyGlyMetCysGlnAsnCysLys 	
	500 1716	91 57	
	480 1656	61 ProLysValLysGluIleIleAspGluArg 	
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	400 1416	1 ProAlaCysHisAspSerAspGluSerAspSerGlyLysAlaValGluValGlnAsnL 	
	380 1356	61 TyrArgLysAlaIleTyrGluValLeuGlnValAlaS 	_
	360 1296	MetProLeuSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsn 	
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701 2317	rArgLeuL
701	TGTCAACC
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ID AAT21884 standard; cDNA to mRNA; 301 BP.
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AC AAT21884;
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14-AUG-1996 (first entry)



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Human gene signature HUMGS03426.
DΕ
          Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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os
           Homo sapiens.
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            01-JUN-1995.
                                              94WO-JP01916.
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            11-NOV-1994;
                                              93JP-0355504.
            12-NOV-1993;
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 XX
             (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
 PA
 PΑ
 ХX
             Matsubara K, Okubo K;
 PI
XX
             WPI; 1995-206931/27.
  DR
             Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
  XX
PT
  PT
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  XX
             Claim 1; Page 991-992; 2245pp; Japanese.
            A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
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               Sequence 301 BP; 96 A; 65 C; 63 G; 66 T; 11 other;
                                                          6.6%; Score 285.2; DB 16; Length 301;
95.3%; Pred. No. 1.5e-48;
vative 0; Mismatches 14; Indels 0;
         Best Local Similarity
         Matches 287; Conservative
                          07
     Db
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     Qy
     Db
                            TAGCAGCAGGAGACGAGAACACCACACAAGACATTTTTCTACAGTATTTCAGGTGCCTA 369
     Οy
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                    121
                            Qу
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Qy 3819 A 3819

Db 301 A 301

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Command line parameters:

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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPPXT=0.5 -FGAPPOP=6 -FGAPEXT=7
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30: em_htg_hum:*
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36: em_htg_wam:*
37: em_htg_wam:*
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41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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/product = "NDA cytosine-5 methyltransferase 3A"
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  Arubse25
Mus musculus DNA cytosine-5 methyltransferase 3A (Dnmt3a) mRNA,
complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                              Xie,S., Okano,M. and Li,E.

Direct Submission

Xie,S., Okano,M. and Li,E.

Direct Submission

Xie,S., Okano,M. and Li,E.

Sidese in to 4192)

Okano,M., Chijiwa,T., Sasaki,H. and Li,E.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-NOV-1999) CVRC, Mass. Gen. Hospital, 149 13th Street, Submitted (04-NOV-1999) USA Sequence update by submitter on Nov 18, 1999 this sequence version replaced gi:3327977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to EST sequences deposited in GenBank
Accession Numbers AA052791, AA111043, AA154890, AA240794,
AA756653, W58898, W59299, W91664, and W91665"
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 4192)
Okano,M., Xie,S. and Li,E.
Cloning and characterization of a family of novel mammalian DNA (cytosine-5) methyltransferases
Nat. Genet. 19 (3), 219-220 (1998)
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/note="contains Cys-rich region"
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IMAGE:3492853,
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Direct Submission

Direct Submission

Submitted (01-MAY-2001) National Institutes of Health, Mammalian Submitted (01-MAY-2001), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Trive, Room 11A03, Bethesda, MD 20892-2590,
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site: http://www-shgc.stanford.edu
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Mus musci
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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RPLASTVNDKLELQECLEHGRIAKFSKVRTITTRSNSIKQGKDQHFPVFMNEKEDILW
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                                                                                                                                     Clone distribution: MGC clone distribution information can be fount through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: RAK Plate: 8 Row: n Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6681208.

1. .4094
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Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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Submitted (25-MAY-1998) CVRC, Mass.
Street, Charlestown, MA 02129, USA
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Sequence update by submitter
On Feb 12, 2001 this sequence version
Location/Qualifiers
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                                                                                                                                   /gene="DNMT3A"
/function="de novo
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/db_xref="taxon:9606"
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AF331856.1 GI:18033252
                 Homo sapiens
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                              Homo sapiens
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Ni,J., Pradhan,S. and Roberts,R.J.
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KEGDDRFFWLFENVVAMGVSDKRDISRFLSNPWTITTPSNGIVGIVGTOCHEDWBNEKDILPGM
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è 8	140 GlyalaSeralaGlyGluGlyLyBGluGlnLyBGlnThrAsnIleGluSerMetLySMet 159	
ò	60 GluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTrpGluSerSerLeuArgGlnArg 1	
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දු ද	180 PrometProArgLeuThrPheGlnAlaGlyAspProTyrTyrIleSerLySArgLySArg 199	
\$ B	200 AspGluTrpLeuAlaArgTrpLysArgGluAlaGluLysLysAlaLysVal11eAlaVal 219 	
\$ 5	20	
ò	40 ProProAlaValGlnGlnProThrAspProAlaSerProThrValAlaThrThrProGlu 259	
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& g	260 ProvalGlyGlyAspalaGlyAspLysAsnAlaThrLy9AlaAlaAspAspGluProGlu 279	
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è 8	320 GlyThrArgTrpValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLys 339	
ò	0 LeuMet ProLeuSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnPro 359	
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Ор	7 TTCCCGGTGTGCCACGACGATGAGAGTGACACTGCCAAGGCCGTGGAGGTGCAGAAC 142	
g 9	400 LysGlnMetileGluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGlu 419	
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16, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 95907 bases at least Q40
Consensus quality: 99223 bases at least Q30
Consensus quality: 101036 bases at least Q20
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AKO25230.1 GI:10437699
oligo capping; fis (full insert sequence).
oligo capping; cion cDNA to mRNA, clone_lib:COL clone:COL06724.
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                                                                                                                                                                                                                                                                                         NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; CDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, Virology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                         Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Humar Genome Center; Shirokane-dai, 4-61, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 2191)
Sugano, S., Suzuki, Y.,
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Okamoto,S., Okitani,R., Ota,T., Suzu
Shibahara,T., Tanaka,T., Nakamura,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                           University of Tokyo
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             /note="highly similar to AF067972 Homo sapiens cytosine methyltransferase 3 alpha (DNMT3A) mR1 505 c 575 g 540 t
                                                                                                                                                      /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="COL06724"
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                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                               /tissue_type="colon"
/clone_lib="COL"
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                                                                                            vector pME18SFL3"
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                                                       PhePheTrpLeuPheGluAsnValAlaMetGlyValSerAspLysArgAspIleSer
                                                                                                        PhePheGluPheTyrArgLeuLeuHisAspAlaArgProLysGluGlyAspAspArgPro
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                                         TTCTTCTGGCTCTTTGAGAATGTGGTGGCCATGGGCGTTAGTGACAAGAGGGACATCTCG
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PRI 08-NOV-2000
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Submitted (24-AUG-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MMO 63108, USA
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Submitted (27-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 168651)
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1 (bases 1 to 168651)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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902 CGATTTCTCGAGTCCAACCCTGTGATGATTGATGCCAAAGAAGTGTCAGGCTGCACACAGG 961
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Homo sapiens BAC clone RP11-179G23 from 2, complete sequence.
AC009474
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                                          787 AlaArgTyrPheTrpGlyAsnLeuProGlyMetAsnArgProLeuAlaSerThrValAsn
                                                                                                                         807 AspLysLeuGluLeuGlnGluCysLeuGluHisGlyArgIleAlaLysPheSerLysVal
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Mulvane, E., Stoneking, T., LaPlant, Y. and McDill, B.
The sequence of Homo sapiens BAC clone RP11-179G23
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Waterston, R.H.
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Waterston, R.H.
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Goegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://pabcpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The clone sequenced to the left is RP11-547F18; the clone sequenced to the left is RP11-547F18; the clone sequenced to the right is RP11-4484, 200 base pair overlap. Actual end of this clone is at base position 18711 of RP11-4464.

Location/Qualifiers

1. .168651
/ Organism="Homo sapiens"
/ db_xref="taxon:9606"
/ map="2"
                                                                                                                         NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by :
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for Genetics, Washington University, St. L.
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H_NH0179G23
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5656. 6129
/rpt_family="MalR"
5205. 6316
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1569. 3760
'rpt_family="MER1_type"
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7819. .7868
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2954. 311.
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6428, 660
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/rpt_family="L1"
7247. .7437
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'rpt_family="L2"
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(615. .1815
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44777 . .44904
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16209. .16345
/note="similar to
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37615
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27140
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37266
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33172.
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9304. .9469
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38006
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35975
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32568
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1719<del>9</del>
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/note="similar to
16210. .16345
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10317. . 10439
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34930. .35230
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32262.
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30824. .31150
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26569. .27058
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19540. .19659
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17575. .18261
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6513. .16676
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13553, .14453
 rpt_family="MIR'
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32775. .33032
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[2219. .12455
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2467. .13537
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5. .46110
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0. .37440
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0. .27647
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444 TyrAlaProProProAlaLysLysProArgLysSerThrThrGluLys----
                                                                                                   GluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGluProProGluGlu 423
                                                                                                                                                          HisAspSerAspGluSerAspSerGlyLysAlaValGluValGlnAsnLysGlnMetIle 403
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                           GAGAAGAATCCCAGCAAAGAAGTTTATGCACACGTGAGGGGTGACCCCTGAGGCAACTGCT
                                                    GluLysAsnProTyrLysGluValTyrThrAspMetTrpValGluProGluAlaAlaAla 443
                                                                                 AGATGGACCTTTGGGGGGGTTCCAGCCTTCTGCCCCCAAGAGACTGGAGCCACAAGAAGAG
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                                                                                                                                                                                                                  AlaIleTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProAlaCys 383
                                                                                                                                                                                                                                                       TTTTGCAGTGTGTTCCACCAGACCAC-CTATAATACAACAAGCAGCCCATGTACCACAAA 75313
                                                                                                                                                                                                                                                                        PheCysSerAlaPheHisGlnAlaThr-----TyrAsnLysGlnProMetTyrArgLys 363
                                                                                                                                                                                                                                                                                                                TGGCTTGGAGA-GGTGAGTTCTCAGTGCTGTGTGTAGAGAAGCTGATACCACTGAGCTCC 75254
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Xie,S., Okano,M. and Li,E.
Direct Submission
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Mus musculus DNA cytosine-5 methyltransferase 3B2 (Dnmt3b) mRNA, alternatively spliced, complete cds.
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                                                                                77078 CATTGAAATTGAAAGGGTATTTGGACTCCCTGTCCATTATACTGACATCTCCAACATAAG 77137
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                                                   717 sGlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrArgLeuLeuHisAspAl 737
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                   -LeuLeuProAsnGlyAspLeuGluLysArgSerGluProGlnProGluGluGl 101
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KDRGEDEESRERAMSEVTNNKGNLEDRCLSCGKKNPVSFHPLFEGGLCQSCRDRFFLEL
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CYMCLPQRCHGVLKERGIKVEKYIASEVCAESIAVGTVWAEGQIKVNDVRKITKKNIEE
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ELQDCLEFSRTAKLKKVQTITTKSNSIRQGKNQLFPVVMNGKDDVLWCTELERIFGFP
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/note="similar to EST sequences deposited in GenBank
Accession Numbers AA116694, AA119979, AA177277, AA210568,
AA407106, and AA575617"
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/function="de novo DNA methylation"
/note="alternatively spliced product; contains Cys-rich
/note="alternatively spliced product; contains Cys-rich
region; C-terminal region is similar to corresponding
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                            eGluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGluProProGluGl
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                                                                                                                                                                                         sAlaIleTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProAlaCy 383
                                                                                                                                                                                                                                                                                                                  GGTACAGTGGTTTGGTGATGGCAAGTTTTCTGAGATCTCTGCTGACAAACTGGTGGCTCT
                                                                                                                                                                                                                                                                                                                                                     pValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yArgGlyPheGlyIleGlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrpTrpPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yAspAlaGlyAspLysAsnAlaThrLysAlaAlaAspAspGluProGluTyrGluAspGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGTACCCCA-----TCAGTTGACTTGAGCCAGGATGGAGATCAGGAGGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lGluGluAsnGlnAlaSerGlyGluSerGlnLysValGluGluAlaSerProProAlaVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTCCGAACCCGACATAGCAATGGGACCTCCAGCTTGGAGAGGCCAAAGAGCCTCCCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGTGCATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACACGAAGGATGCTCC
                                                                                                                                                       GGCCATGTACCACACTCTGGAGAAAGCCAGGGTTCGAGCTGGCAAGACCTTC------
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                                                                                                               sHisAspSerAspGluSerAspSerGlyLysAlaValGluValGlnAsnLysGlnMetIl
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1008

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303 948 283 888 263 786

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840 243 203 681 183

726

-GAAAGCCCGGC

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570 146

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<u>ک</u> ۾	442	aalatyralaproproproproalaLysLysProArgLysSerThrThrGluLysProLy 462 	
8 6	462	BValLysGluIlelleAspCluArgThrArgGluArgLeuValTyrGluValArgGlnLy 482 	
y d	60 0	GCYSATGABUILEGIUME GAAGGGCAATCTGGAAGACCCTGTTTGTCCTGTGGAAAGAAGAACCCTGTGTCCTTCA	
ò a	502	SProLeuPheIleGlyGlyMetCysGlnAsnCysLysAsnCysPheLeuGluCysAlaTy 522	
è 6	522	rGlnTyraspappapGlyTyrGlnSerTyrCysThrIleCysCysGlyGlyargGluVa 542 	
상 임	542	LeumetCysGlyAsnAsnCysCysArgCysPheCysValGluCysValAspLeuLe 562 	
8 6	562	uValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTrpAsnCysTyrMetCy 582	
S G	582	BG1yHisLysG1yThrTyrG1yLeuLeuArgArgArgArgG1uAspTrpProSerArgLeuG1 602 	
S do	602	nMetPhePheAlaAsnAsnHisAepGlnGluPheAspProProLysValTyrProPr 621	
ک او	621	oValproAlaGluLysArgLysProIleArgValLeuSerLeuPheAspGlyIleAlaTh 641 :::	
è 8	641	rGlyLeuLeuValLeuLysAspLeuGlyIleGlnValAspArgTyrIleAlaSerGluVa 661 GGGGTACTTGGTGCTCAAGGAGTTGGGTATTAAAGTGGAAAAGTACATTGCTCCGAAGT 2043	
ò q	661	CysGluaspserlleThrValGlyMetValargHisGlnGlyLysIleMetTyrValGl 681 	
95 95	681	yaspvalargservalThrGlnLysHisIleGlnGluTrpGlyProPheAspLeuValll 701 	
è 8	701	eGlyGlySerProCysAsnAspLeuSerIleValAsnProAlaArgLysGlyLeuTyrGl 721 	
ò 8	721	uGlyThrGlyArgLeuPhePheGluPheTyrArgLeuLeuHisAspAlaArgProLysGl 741 	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROD 08-JUN-2000
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Gene="Dnmc3b"

/function="methylates cytosine in DNA"

/note="alternatively spliced"

/codon start="

/product="DNA cytosine-specific methyltransferase isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 4278)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
P.R.China
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Ynn, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
Shen, Y.
                                                                                                                                                                                                                                                                                                                                                                                                         2464 GATGGCTTCAAAGAATGATAAGCTCGAGCTGCAGGACTGCCTGGAGTTCAGTAGGACAGC 2523
                                                                                                                                                                                        2524 AAAGTTAAAGAAAGTGCAGACAATAACCACCAAGTCGAACTCCATCAGACAGGGCAAAAA 2583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cloning of full-length Dnmt3b cDNA and its alternative splicing
                        2404 GTCTGCTGCTGCTGCTCACAGGGCCCGGTACTTCTGGGGTAACCTACCCGGAATGAACAGGCCCGT 2463
                                                                                                                                                                                                                                                                      2644 AAGGATCTTCGGCTTCCCTGCTCACTACACGGACGTGTCCAACATGGGCCGCGCGCCCG 2703
                                                                                                                                                             821 aLysPheSerLysValArgThrIleThrThrArgSerAsnSerIleLysGlnGlyLysAs 841
                                                                             801 uAlaSerThrValAsnAspLysLeuGluLeuGluCysLeuGluHisGlyArgIleAl 821
                                                                                                                                                                                                                                           841 pGlnHisPheProValPheMetAsnGluLysGluAspIleLeuTrpCysThrGluMetGl 861
                                                                                                                                                                                                                                                                                                                                861 uArgValPheGlyPheProValHisTyrThrAspValSerAsnMetSerArgLeuAlaAr 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A278 bp mRNA linear ROD 08-JUN. Mus musculus DNA cytosine-specific methyltransferase isoform 2 (Dnmt3b) mRNA, complete cds.
781 | ISErAlaAlaHisArgAlaArgTyrPheTrpGlyAsnLeuProGlyMetAsnArgProLe 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
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1. .4278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoforms in mouse embryonic tissue Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
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1. .4278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="Dnmt3b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         901 uLysGlufyrPheAlaCys 907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF151970
AF151970.1 GI:8347119
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Mus musculus
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LTRETKDTRTRSESPAVRTRHSNGTSSLERQRASPRITRGRQGRHHVQEYPVEFPATR
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Percent Similarity:
Best Local Similarity:
Query Match: BASE COUNT ORIGIN US-09-720-086-5 (1-908) x AF151970 (1-4278) ment Scores: 405 345 534 121 525 101 285 165 594 141 465 163 144 84 77 57 38 19 4. AspArgLysGluGlyGluGluGluGluAsnArgGly-LysGluGluArgGlnGluPr 38 gGlyArgLeuArgGlyGlyLeuGlyTrpGluSerSerLeuArgGlnArgProMetProAr AAAGCTCACCCGTGAGACCAAGGACACCAGGACGCGCTCT aSerAla----oProGluAlaSerArgAlaValGluAsnGlyCysCysValThrLysGluGlyArgGlyAl 141 ySerProAlaAlaGlyGlnLysGlyGlyAlaProAlaGluGlyGluGlyThrGluThrPr 121 GGAGTGCATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACACGAAGGATGCTCC 524 GGAAACAATGAAGGGAGACAGCAGACATCTGAATGAAGAAGAGGGTGCCAGCGGGTATGA 464 nAspSerGlyProSerAsp------CGCGGGATCTCCCCTCCCCCATCCATAGTGCCTTGGGACCAAATCCAGGGCCTTCTTTCA 404 CGACAGGCCCGCTGAGGCTTGTGCCAGACCTTGGAAACCTCAGGTATATACCTTTCCAGA 344 oSerAlaThrAlaArgLysValGlyArgProGlyArgLysArgLysHisPro---ProVa 57 AGCGGCCCAAGTAAACGTAGCGCAGCGATCGGCGCCGGAGATTCGCGAAACCCGACACTCC 224 SerGlyProGlyAspThrSerSerSer-----SerLeuGluArgGluAsp 18 -----LeuLeuProAsnGlyAspLeuGluLysArgSerGluProGlnProGluGluGl 101 lGluSerSerAspThrProLysAspProAlaValThrThrLysSerGlnProMetAlaGl 77 AGGAGATGGAGACAGATGATGAAGTAGATGATGGGAATGGCTCTGATATTCTAATGCC AÄĞCTCCCGGCTGTCTAAGAGGGAGGTCTCCAGCCTTCTGAATTACACGCAGGACATGAC AGTCTTGGAGGCAATCTGCACAGAGCCAGTCTGCACACCAGAGACCAGAGGCCGCAGGTC ------LysGluGlnLysGlnThrAsnIleGluSerMetLysMetGluGlySerAr 163 -GlyGluGly----1055 a ELQDCLEFSRTAKLKKVQTITTKSNSIRQGKNQLFPVVMNGKDDVLWCTELERIFGFPAHYTDVSNMGRGARQKLLGRSWSVPVIRHLFAPLKDYFACE" 1.6e-90 2211.00 61.22% 46.95% 45.04% ი Gaps: Length: Matches: Indels: Mismatches: Conservative: 956 t -----cc 4278 454 138 266 109 -GAAAGCCCGGC 764 183 653 713 146 143 593 533 83

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765 TGTCCGAACCCGACATAGCAATGGGACCTCCAGCTTGGAGAGGCAAAGAGCCTCCCCCAG

542 1826	22 rGlnTyrAspAspAspGlyTyrGlnSerTyrCysThrIleCysCysGlyGlyArgGluVa 	Qy 5 Db 17	
522 1766	02 sProLeuPheIleGlyGlyMetCysGlnAsnCysLysAsnCysPheLeuGluCysAlaTy	Оу 5 Въ 17	
502 1706	82 SCYSARGASNIleGluASPIleCySIleSerCYSGlYSerLeuAsnValThrLeuGluHi ::: 47 CAAGGGCAARCTGGAAGACCGCTGTTGTCCTGTGGAAAGAAGAACCCTGTGTCCTTCCA	Qy 4 Db 16	н о
482 1646	62 sValLysGluIleIleAspGluArgThrArgGluArgLeuValTyrGluValArgGlnLy : : : :	Qy 4 Db 15	
462 1595	42 AAlaTyrAlaProProProProAlaLysLysProArgLysSerThrThrGluLysProLy	Qy 4 Db 15	n 0
442 1535	23 uGluLysAsnProTyrLysGluValTyrThrAspMetTrpValGluProGluAlaAl ::::	Qy 4 Db 14	
423 1490	03 eGluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGlyLeuGluProProGluGl : ::: :	Qy 40 Db 143	
403 1430	83 sHisAspSerAspGluSerAspSerGlyLysAlaValGluValGlnAsnLysGlnMetIl	Qy 3 рь 13	
383 1383	63 sAlaIleTyrGluValLeuGlnValAlaSerSerArgAlaGlyLysLeuPheProAlaCy	Qy з рь 13	
363 1331	43 uSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLy	Qy 3. Db 12	п о
343 1271	23 pValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLe	Qy 3; Db 12;	н о
323 1211	03 oGlyArgIleValSerTrpTrpMetThrGlyArgSerArgAlaAlaGluGlyThrArgTr 	QУ 3	п о
303 1151	83 yArgGlyPheGlyIleGlyGluLeuValTrpGlyLysLeuArgGlyPheSerTrpTrpPr ::: :::	Qy 2 рь 10	п О
283 1091	63 YASDALAGIYASDLYSASNALATHYLYSALAALAASDASDGluPrOGluTyrGluAspGl	Qy 2 рь 10:	
263 1031	43 lGlnGlnProThrAspProAlaSerProThrValAlaThrThrProGluProValGlyGl	Qy 2:	п о
243 983	23 lGluGluAsnGlnAlaSerGlyGluSerGlnLysValGluGluAlaSerProProAlaVa	Qy 2: Db 9:	п о
929	03 uAlaArgTrpLysArgGluAlaGluLysLysAlaLysValIleAlaValMetAsnAlaVa ;;; 70 TGTGGAGTTTCCGGCTACCAGGTCTCGGAGACGTCGAGCATCGTCTTCAGCAAGCA	Оу В В	п о
6 6	GLeuThrPheGlnAlaGlyAspProTyrTyrIleSerLysArgLysArgAspGluTrp 	8 1	

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WNGKDDVLMCTELERIFGFPAHYTDVSNMGRGARQCLGRSWSVPVIRLLFAPLKDYP
                                                                                                                                      AF068626 4195 bp mRNA linear ROD 06-DEC-1999 Mus musculus DNA cytosine-5 methyltransferase 3B1 (Dnmt3b) mRNA, alternatively spliced, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xie,S., Okano,M. and Li,E.
Direct Submission
Submitted (28-MX)-1998) CVRC, Mass. Gen. Hospital, 149 13th Street,
Charlestown, MA 02129, USA
3 (Dases 1 to 4195)
Okano,M., Chijiwa,T., Sasaki,H. and Li,E.
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Cloning and characterization of a family of novel mammalian DNA (cytosine-5) methyltransferases (cytosine-5) methyltransferases Mat. Genet. 19 (3), 219-220 (1998)
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Accession Numbers AA116694, AA119979, AA17277, AA210568,
AA407106, and AA575617"
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Sequence update by submitter
On Nov 18, 1999 this sequence version replaced gi:3327979.
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AF068626.2 GI:6449469
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727 TGTGGAGTTTCCGGCTACCAGGTCTCGGAGACGTCGAGCATCGTCTTCAGCAAGCA		TCTGA LysMe	Qy 121 oProGluAlaSerArgAlaValGluAsnGlyCysCysValThrLysGluGlyArgGlyAl 141	Qy 84LeuLeuProAsnGlyAspLeuGluLysArgSerGluProGlnProGluGluGl 101 Db 322 GGAGTGCATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACACGAAGGATGCTCC 381 Qy 101 ySerProAlaAlaGlyGlnLysGlyGlyAlaProAlaGluGlyGluGlyThrGluThrPr 121 Db 382 CTCACCC	Qy 57 IGluSerSerAspThrProLysAspProAlaValThrThrLysSerGlnProMetAlaGl 77	Q 19 AspArgLysGluGlyGluGluGluGluAsmArgGly-LysGluGluArgGlnGluPr 38	Gaps: 09-720-086-5 (1-908) x AF068626 (1-4195) 4 SerGlyProGlyAspThrSerSerSerSe	BASE COUNT 1061 a 1059 c 1125 g 950 t ORIGIN Alignment Scores: Pred. No.: 2.62e-90 Length: Score: Score: 206.00 Matches: 455 Percent Similarity: 59.78* Best Local Similarity: 46.10* Query Match: 10 Indels: 119
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AF151969.1 GI:8347117

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4338 bp mRNA linear ROD 08-JUN-2000 Mus musculus DNA cytosine-specific methyltransferase isoform 1 AP151969
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Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="DNA cytosine-specific methyltransferase isoform
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                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 4338)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and Shen, Y.
                                                                                                                                                                                                                                                              Cloning of full-length Dnmt3b cDNA and its alternative splicing
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2 (bases 1 to 4338)
Yin, B., Chen, Y. T., Zhu, M., Luo, Y. J., Zhu, N., Xu, S. C., Wu, G. Y.
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                    pValMetTrpPheGlyAspGlyLysPheSerValValCysValGluLysLeuMetProLe 343
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                                                                                           oGlyArgIleValSerTrpTrpMetThrGlyArgSerArgAlaAlaGluGlyThrArgTr 323
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27 AATTCCTGCAGCCAAAAGGAGGCCCATTAGAGTCCTGTCTCTGTTTGATGGAATTGCAAC 21	_
Pr	Q Q
67 AGACTTCTTCACTACTGATCCTGACCTGGAAGAATTTGAGCCACCCAAGTTGTACCCAGC 21	B
602 nMetPhePheAlaAsnAsnHisAsnGlnGluPheAsnProProLvsValTvrProPr	
582 sGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgGluAspTrpProSerArgLeuGl 602 :::	망 <i>와</i>
47 GGTGGGCAGGCACAGCTGAGGATGCCAAGCTGCAGGAACCCTGGAGCTGCTATATGTG 20	Db 1
562 uValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTrpAsnCysTyrMetCy 582	γQ
	Db 1
LeuMetCysGlyAsnAsnAsnCysCysArgCysPheCysValGluCysValAa	νο
27 CATGTATGATGAGGACGGCTATCAGTCCTACTGCACCGTGTGCTGCAGGGCCGTGAACT 18	뫄.
GlnTvrAspAspAspGlvTvrGlnSerTvrCvsThrIleCvsCvsGlvGlvArqGluVa 54	8
67 CCCCCTCTTTGAGGGTGGGCTCTGTCAGAGTTGCCGGGATCGCTTCCTAGAGCTCTTCTA 18	Db 1
502 sProLeuPheIleGlyGlyMetCysGlnAsnCysLysAsnCysPheLeuGluCysAlaTy 52	
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nlleGluAspIleCysIleSerCysGlySerLeuAsnValThrLeuGl	Ş
ð	
ValLysGluIleIleAspGluArgThrArgGluArgLeuValT	8
1596 TGCTTCTGAGTCCCCCCCCACCCAAGCGCCTCAAGACAATAGCTATGGCGGGAAGGACCG 1655	Db 1
ProProAlaLysLysProArgLysSerThrThrGluLysPi	γŞ
1 1 1 1 1 1 1	Db 1
422 uGluGluLysAsnProTyrLysGluValTyrThrAspMetTrpValGluProGluAlaAl 442	8
CAGTAGGAAC	-
421	Q
1431 GGAGTGGGCCCACGGTGGCTTCAAGCCTACTGGGATCGAGGGCCTCAAACCCAACAAGAA 1490	•
GluTrpAlaLeuGlyGlyPheGlnProS	ργ
AGTCCTGGAGAGTCACTGGAGGACCAGCTGAAGA	
383 sHisAspSerAspGluSerAspSerGlyLysAlaValGluValGlnAsnLysGlnMetIl 403	Qy
1332 GGCCATGTACCACACTCTGGAGAAAGCCAGGGTTCGAGCTGGCAAGACCTTC 1383	
\mathbf{H}	δ
72 GGGGCTGTTCAGCCAGCACTTTAATCTGGCTACCTTCAATAAGCTGGTTTCTTATAGGAA 13	망 .
343 uSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLy 363	Q

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F151974 4163 bp mRNA linear ROD 08-JUN-2000 lus musculus DNA cytosine-specific methyltransferase isoform 6 DNMt3b) mRNA, complete cds.
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Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 4163)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
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Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and Shen, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cloning of full-length Drmt3b cDNA and its alternative splicing isoforms in mouse embryonic tissue Unpublished
                                                                 2426
                                                                                                                     2486
                                                                                                                                                             TCAGAAGCTGCTGGGCAGGTCCTGGAGTGTACCGGTCATCAGACCTGTTTGCCCCCTT 2966
2727 AAAGTTAAAGAAAGTGCAGACAATAACCACCAAGTCGAACTCCATCAGACAGGGGAAAAA 2786
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                                                                                                                                                                                                                                                                                                                                                                                                                    pGlnHisPheProValPheMetAsnGluLysGluAspIleLeuTrpCysThrGluMetGl 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uArgValPheGlyPheProValHisTyrThrAspValSerAsnMetSerArgLeuAlaAr 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gGlnArgLeuLeuGlyArgSerTrpSerValProValIleArgHisLeuPheAlaProLe 901
                                                                  regregaageccarecaargarcrereraacgreaarccreeccecaaaggrirararda
                                                                                                               uGlyAspAspArgProPhePheTrpLeuPheGluAsnValValAlaMetGlyValSerAs
                                                                                                                                                                                                                      eGlyGlySerProCysAsnAspLeuSerIleValAsnProAlaArgLysGlyLeuTyrGl
                                                                                              uGlyThrGlyArgLeuPhePheGluPheTyrArgLeuLeuHisAspAlaArgProLysGl
                                                                                                                                                                                                  pLysArgAsplleSerArgPheLeuGluSerAsnProValMetIleAspAlaLysGluVa
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SEISADKLVALGGESQHFWLATFWKLVSYRKAMYHTLERKRYRAKKTFSSSPGESLED
QLKFMELWAHGGFKFTGIEGLKPWKKOPENKSRRYTUNDSAGESPPRRLKTNSYG
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1074 c 1128 g 929 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRRRRASSSASTPWSSPASVDFWEEVTPKSVSTPSVDLSQDGDQEGMDTTQVDAESIY
GDSTEYQDDXEFGIGDLVWGKIKGPSWWPAMVVSWKATSKRQAMPGMRWVQWFGDGKF
                                                                                                                                                                                                                                                                                                            'codon_start=1
product="DNA cytosine-specific methyltransferase isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 ACAGAGCCAGTCTGCACACCAGAGACCAGAGCCGCAGGTCAAGCTCCCGGCTGTCTAAG 497
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309 AGCAGACATCTGAATGAAGAAGAGGTGCCAGCGGTATGAGGAGTGCATTATCGTTAAT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 GlyAspLeuGluLysArgSerGluProGlnProGluGluGlySerProAlaAlaGlyGln 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 LysGlyGlyAlaProAlaGluGlyGluGlyThrGluThrProProGluAlaSerArgAla 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 CGCACGGGCGCTCCAGTCCGGCAGCGCCGGGGTTAAGCGGCCCCAAGTAAACGTAGCGCAG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 -----HisProProValGluSerSerAspThrProLysAspProAlaValThrThrLys 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 ĠĠĠAACTTCAGTGACCAGTĊĊTCAGACACGAAGGATGCTCCCTĊÀĊĊĊ------
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                                                                                                                                                                                                                                                       /function="methylates cytosine in DNA'
/note="alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                 db_xref="taxon:10090"
'dev_stage="8-9 day old embryo"
...4163
                                                  'organism="Mus musculus"
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Location/Qualifiers
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'qene="Dnmt3b"
                                                                                                                                                                               'gene="Dnmt3b"
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488	469 GluArgThrArgGluArgLeuValTyrGluValArgGlnLysCysArgAsnIleGluAsp	Qy
1490	40 CCCAAGCGCCTCAAGACAAATAGCTATGGCGGGAAGGACCGAGGGGGAG	Db 14
468	laLysLysProArgLysSerThrThrGluLysProLysValLysGluIleIle	Q
4	95 CGAAGACGCACAACCAATGACTCTGCTGCTTCTGAGTC	<u> </u>
448	29 LysGluValTyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProProPr	Qy 4
428 1394	10 PhedinProSerGlyProLySGLyLeuGLuProProGluG ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :: :: :::	Db 13
μ U	/S AGTCCTGGAGAGTCACTGGAGGCCCATGCTGGAGTGGGCCCX	-
40	90 AspSerGlyLysAlaValGluValGlnAsnLysGlnMetIleGluTrpAlaL	
1274	36 GAGAAAGCCAGGGTTCGAGCTGGCAAGACCTTC	Db 12
389	sLeuPheProAlaCysHisAspSerAspGluSe 	8
369 1235	SO PheHisGlnAlaThrTyrAsnLysGlnProMetTyrArgLysAlaIleTyrGluValLeu 	Оу 3 Db 11
1175		7
349	30 GlyLysPheSerValValCysValGluLysLeuMetProLeuSerSer)
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329	10 TrpMetThrGlyArgSerArgAlaAlaGluGlyThrArgTrpValMetTrpPheGly	Qy 3
1055	96 GACCTCGTGTGGGGAAAGATCAAGGGCTTCTCCTGGTGGCCTGC	Db 9
309	90 GluLeuValTrpGlyLysLeuArgGlyPheSerTrpTrpProGlyArgIleValSe	0у 2
9	36 GCAGAGAG	
œ	70 AlaThrLysAlaAlaAspAspGluProGluTyrGluAspGlvArqGlvPheGlvIle	
93	.:::::::::::::::::::::::::::::::::::::	
269	50 AlaSerProThrValAlaThrThrProGluProValGlyGlyAspAlaGlyAspLys	0у 2
878	34 GTCGACTTCATGGAAGAAGTGACACCTAAGAGCGTCAGTACCCCCA	Db 8
249	30 GlyGluSerGlnLysValGluGluAlaSerProPro	Qy 2
833	74 AGGTCTCGGAGACG	2 م ^ر م
229	10 AlaGluLysLysAlaLysValIleAlaValMetAsnAlaValGluGluAsnGlnAlaSe	Ωу 2
7	29 GGCCGCCATGTGCAGGAGTACCCTGTGGAGTTTCCGGCTA	7.7 Mg
209	90 AspProTyrTyrIleSerLysArgLysArgAspGluTr	Qy)
728	69 AATGGGACCTCCAGCTTGGAGAGGCAAAGAGCCTCCCCCAGAATCACCCGAGGTCGGCA	Db 6
189	70 LeuGlyTrpGluSerSerLeuArgGlnArgProMetProArgLeuThrPl	0у 1
668	18 AAGGACACCAGGACGCGCTCTGAAAGCCCGGCTGTCCGAACCCGGACATAG	Db 6
169	50 LysGlnThrAsnIleGluSerMetLysMetGluGlySerArgGlyArgL	0у 1
617	:: Second of the control of the con	Db 5
149		9
557	98 AGGGAGGTCTCCAGCCTTCTGAATTACACGCAGGACATGACAGGAGATGGAGA	Db 4
146	44GlyGluGly	Qy 1

828 ThrileThrThrArgSerAsnSerIleLysGlnGlyLysAspGlnHisPheProValPhe 847	8
808 LysLeuGluLeuGlnGluCysLeuGluHisGlyArgIleAlaLysPheSerLysValArg 827	B 6
788 ArgTyrPheTrpGlyAsnLeuProGlyMetAsnArgProLeuAlaSerThrValAsnAsp 807	P 9
768 PheLeuGluSerAsnProValMetIleAspAlaLysGluValSerAlaAlaHisArgAla 787	B &
heG1w CGAG	B 8
728 PheGluPheTyrArgLeuLeuHisAspAlaArgProLysGluGlyAspAspArgProPhe 747	B 8
708 AspleuSerIleValAsnProAlaArgLysGlyLeuTyrGluGlyThrGlyArgLeuPhe 727 	유 성
688 GlnLysHisIleGlnGluTrpGlyProPheAspLeuValIleGlyGlySerProCysAsn 707 ::: ::: :	å S
668 ValGlyMetValArgHisGlnGlyLysIleMetTyrValGlyAspValArgSerValThr 687 :: ::	유 성
648 AspLeuGlyIleGlnValAspArgTyrIleAlaSerGluValCysGluAspSerIleThr 667 : ::::	P Q
628 LysProlleArgValLeuSerLeuPheAspGlylleAlaThrGlyLeuLeuValLeuLys 647 :::	유 성
609 HisaspGlnGluPheAspProProLysValTyrProProValProAlaGluLysArg 627	D
589 GlyLeuLeuArgArgArgGluAspTrpProSerArgLeuGlnMetPhePheAlaAsnAsn 608 ::: ::: 1851 GGGTCCTCCGACGCAGGAAAGATTGGAACATGCGCCTGCAAGACTTCTTCACTACTGAT 1910	g &
569 GlnAlaAlaIleLysGluAspProTrpAsnCysTyrMetCysGlyHisLysGlyThrTyr 588 :::	8 8
549 AsnCysCysArgCysPheCysValGluCysValAspLeuLeuValGlyProGlyAlaAla 568	B 8
529 TyrGlnSerTyrCysThrIleCysCysGlyGlyArgGluValLeuMetCysGlyAsnAsn 548	₽ 8
509 MetCysGlnAsnCysLysAsnCysPheLeuGluCysAlaTyrGlnTyrAspAspAspGly 528	B &
489 IleCysIleSerCysGlySerLeuAsnValThrLeuGluHisProLeuPheIleGlyGly 508	DB Q9
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Nuzny, D. M., Adang, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Anderatunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bange, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Branch, M.C., Burch, P., Burkett, C., Burch, B., Brown, M., Bryant, N.E., Burch, P., Burkett, C., Burch, E., Brown, M., Bryant, N.E., Charler, M., Cavazos, S.R., Chacko, J., Ghavez, D., Chen, R., Chen, R., Chock, J., Christopoulos, C., Chen, R., Cor, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, R., David, M.L., Davis, C., Edgard, C., Escotto, M., Earnhart, C., Edgard, D., Garcia, A., Garner, P., Hamilton, K., Harris, K., Hart, M., Havlak, P., Hahe, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hahe, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hahe, S., Hamilton, K., Karloson, E., Kally, S., Mhan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kuly, S., Mhan, U., King, L., Luna, R., Martinez, M., Martinez, M., Martinez, M., Martinez, M., Martinez, M., Martinez, M., Martinez, Decrey, J., Li, J., Li, J., Liu, J., Liu, M., Martinez, M., Martinez, M., Martinez, M., Martinez, D., Wartinez, D., Wartinez, D., Wartinez, D., Wartinez, D., Wartinez, D., Wartinez, D., Waltinez, D., Waltinez
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Rattus norvegicus clone CH230-28122, *** SEQUENCING IN PROGRESS
***, 65 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                 2690
                                                                                                                                                                                                                                    2691 GCTCACTACACGGACGTGTCCAACATGGGCCGCGGGGGCCCGTCAGAAGCTGCTGGGCAGG 2750
                                                                                                                                                                                                                                                                                                                                                                         2751 TCCTGGAGTGTACCGGTCATCAGACACCTGTTTGCCCCCTTGAAGGACTACTTTGCCTGT 2810
2511 ACAATAACCACCAAGTCGAACTCCATCAGACGGCCAAAACCAGCTTTTCCCTGTAGTC 2630
                                                                                                                                                                                                                                                                                                                                    888 SerTrpSerValProValIleArgHisLeuPheAlaProLeuLysGluTyrPheAlaCys 907
                                                           848 MetAsnGluLysGluAspIleLeuTrpCysThrGluMetGluArgValPheGlyPhePro
                                                                                                   2631 ATGAATGGCAAGGACGACGTTTTGTGGTGCACTGAGCTCGAAAGGATCTTCGGCTTCCCT
                                                                                                                                                                                                   868 ValHisTyrThrAspValSerAsnMetSerArgLeuAlaArgGlnArgLeuLeuGlyArg
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Rattus norvegicus
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AC112586
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JOURNAL
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Worley, K.C. Direct Submission

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tcm.cdu/docs/genbank draft data.html).

NOTE: This is a working draft' sequence. It currently consists of 65 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                 Norley, K.C.

Direct Submission

Direct Submission

Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza Houston, TX 77030, USA

On Jul 12, 2002 this sequence version replaced gi:20303171.

Center: Baylor College of Medicine

Center: Baylor College of Medicine

Center code: BCM

Center code: BCM
Submitted (22-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 176697)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: GRAT
Center clone name: CH230-28122
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 121959 bases at least Q40
Consensus quality: 126371 bases at least Q20
Consensus quality: 130428 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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1 (bases 1 to 4335)
Ni,J., Pradhan,S. and Roberts,R.J.
Cloning, expression and characterization of human DNMT3 genes
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Ni,J., Pradhan,S. and Roberts,R.J.
Direct Submission
Submitted (22-DEC-2000) New England Biolabs, 32 Tozer Road,
Beverly, MA 01915, USA
Location/Qualifiers
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1555 GATGAA-----GATCAGAGCCCGAGAACAAATGGCTTCAGATGTTGCCCAACAACAACAAG 1605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTACG----CCCGCCTAGCCCAGGACAGCCAGCAGGGGGGGCATGGAGTCCCCGCAG-GTG
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                                                                                           TyrAspAspAspGlyTyrGlnSerTyrCysThrIleCysCysGlyGlyArgGluValLeu
                                                                                                                                              CTCTTTGAGGGGGGCTCTGTCAGACATGCCGGGATCGCTTCCTTGAGCTGTTTTACATG 1725
                                                                                                                                                                                                                       AGCAGCCTGGAAGATGGCTGTTTGTCTTGTGGCAGGAAAAACCCCCGTGTCCTTCCACCCT
                                                                                                                                                                                                                                                                                                                                                                            TACTGCCCCGCACCCAAGCGCCTCAAGACAAATTGCTATAACAACGGCAAAGACCGAGGG 1554
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De 1144 GCCCCAGCCCAAACCCCCCACCCAAGCCTTCAACCCCCCAAGCCTGAACCTGAACCCTCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCCAAGCCTGAACCTGAACCTGAACCTGCAACCTGCAACCTGAACCTGCAACCACGCCAACCTGCAACCATGCAACCAAC
84 GLACAGOGCANAGOGCANGCCANCOCTONGAGCCCANGACTOTHANGCTPTPANTCYSTYPMETCYSTIP

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396 GACCTCGTGTGGGGAAAAATCAAGGCTTCTCCTGGTGGCCTGCCATGGTGGTGTCCTGG 1055
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                                                                                     250 GGCGCGATCGCGGCGCCGCGTACAGCCAGCCTCA-CGACAGGAAACAATGAAGGGAGAC 308
                                                                                                                                                                                                                                                               309 AGCAGACATCTGAATGAAGAAGAGGTGCCAGCGGGTATGAGGAGTGCATTATCGTTAAT 368
                                                                                                                                                                                                                                                                                                     88 GlyAspLeuGluLysArgSerGluProGlnProGluGluGluGlySerProAlaAlaGlyGln 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 LysGlnThrAsnIleGluSerMetLysMetGluGlySerArgGlyArgLeuArgGlyGly 169
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                                                                                                                                             936 GCAGAGAGCATATAGGAGACAGCACAGAGTATCAGGATGATAAAAGAGTTTGGAATAGGT 995
                                                            54 -----HisProProValGluSerSerAspThrProLysAspProAlaValThrThrLys 71
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               4223 bp mRNA linear ROD 08-JUN-2000 Mus musculus DNA cytosine-specific methyltransferase isoform 5 (Dnnmis) mRNA, complete cds.
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SEISADKLVALGLESQHFNLATFNKLVSYRKAMVHTLERARVRAGKTPSSSPGESLED
OLKPMLEWAHGGFKPFGIEGLKPNKKOPVNKSKVRRSDSRNLEPRRREMKSRRTTN
DSAASESP PPRKLKTVSYGGKDRGEDESRERNASEVTNKGNLEDRCLSCGKKNPVS
FHPLFBGGLCQSCRDRFLELFYMYDBDGYQSYCTVCCGGRELLLCSNTSCCRCFCVEC
LEVLUGAGGTABDAKLOPPWGSVMCLPORCHVLEKGGIKDRKDNRMSLODFFTTDPDLEBFEP
PKLYPALPAAKRRPIFVLSLFDGIATGYLVLKELGIKUBKYIASBVCAESIAVGTVKH
EGOIKYVNDVRKITKKNIEBMGPFDLVIGGSPCNDLSNVNPARKGLYBGTGRLFFEFY
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ATCTEPVCTPETRGRRSSSRLSKRESSELSKESSELDAPK
LTTREVTCHTPRESPANTTRIBIOGTSSLLENGTRAPPRINGSDBDVDDGNGSDILMPK
LTRETKCHTRRESPANTTRIBIOGTSSLERGRAPPRITRGRQCRHHVQEYPVEFPATR
SRRRRASSSASTPWSSPASVDPMEEVTPKSVSTPSVDLGQDGDQBGMDTTQVDABSIY
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FWGNLPGMNRPVMASKNDKLELQDCLEFSRTAKLKKVQTITTKSNSIRQGKNQLPPVV
MNGKDDVLWCTELERIFGFFAHYTDVSNMGRGARQKLLGRSWSVPVIRHLFAPLKDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (17-MAY-1999) Department of Biochemistry and Molecular Biology, Institution of Basic Medical Sciences, Chinese Academy of Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'codon_start=1
'product="DNA cytosine-specific methyltransferase isoform
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 4223)
Tin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
                                                                                                                                                                                                                                                                                           Cloning of full-length Dnmt3b cDNA and its alternative splicing isoforms in mouse embryonic tissue Upublished 2 (2 Chen, Y. T., Zhu, M., Luo, Y. J., Zhu, N., Xu, S. C., Wu, G. Y. and Yin, B., Chen, Y. T., Zhu, M., Luo, Y. J., Zhu, N., Xu, S. C., Wu, G. Y. and
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/note="alternatively spliced"
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Mismatches:
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db_xref="taxon:10090"

dev_stage="8-9 day old embryo"
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/organism="Mus musculus"
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db_xref="GI:8347128"
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'qene="Dnmt3b"
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                                                                                                                                                           Hisasp---GlnGluPheAspProProLysValTyrProProValProAlaGluLysArg
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TATCAGTCCTACTGCACCGTGTGCTGTGAGGGCCGTGAACTGCTGCTGCAGTAACACA 179
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GTGGGAACTGTTAAGCATGAAGGCCAGATCAAATATGTCAATGACGTCCGGAAAATCACC
              ValGlyMetValArgHisGlnGlyLysIleMetTyrValGlyAspValArgSerValThr
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                                         GCTCACTACACGGACGTGTCCAACATGGGCCGCGCGCCCCTCAGAAGCTGCTGGGCAGG
                                                      ValHisTyrThrAspValSerAsnMetSerArgLeuAlaArgGlnArgLeuLeuGlyArg
                                                                                                                               LysLeuGluLeuGlnGluCysLeuGluHisGlyArgIleAlaLysPheSerLysValArg
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TCCTGGAGTGTACCGGTCATCAGACACCTGTTTGCCCCCTTGAAGGACTACTTTGCCTGT
          SerTrpSerValProValIleArgHisLeuPheAlaProLeuLysGluTyrPheAlaCys
                                                                                      ATGAATGGCAAGGACGACGTTTTGTGGTGCACTGAGCTCGAAAGGATCTTCGGCTTCCCCT
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Human polynucleoti	Human immune syste	Human genome-deriv		#15827 used	Probe #11791 for g	Human bone marrow	Ф	for		Human breast cell	Mouse spliced tran	Human polynucleoti	Human genome-deriv	Probe #2405 used t	#2546 used	for	Human bone marrow		Probe #2427 for ge		Human breast cell	Human ovarian canc	Human ovarian canc	ncer r		Human cDNA clone (Human ORFX ORF3010	Human DNA methyltr	Human polynucleoti	Human nervous syst	DNA encoding novel	Human nervous syst		Receptor #25 parti	DNA encoding novel

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AAZ37095 standard; DNA; 4192 BP

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CDS 25-JUN-1998; 24-JUL-1998; Mus sp. carcinoma; sarcoma; leukaemia; DNA methylation; ss. De novo DNA cytosine methyltransferase; Dnmt3a; neoplastic disorder; DNA encoding de novo DNA cytosine methyltransferase Dnmt3a 27-MAR-2000 (GEHO) GEN HOSPITAL CORP 25-JUN-1999; 29-DEC-1999. WO9967397-A1 (first entry) 98US-0090906 98US-0093993 99WO-US14373 /*tag= a /product= "de novo DNA cytosine methyltransferase /product= "de novo DNA cytosine methyltransferase Location/Qualifiers 217..2943

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The present sequence encodes a murine de novo DNA cytosine
methyltransferase designated Dnmt3a. The polypeptides can be administered
methyltransferase designated Dnmt3a. The polypeptides can be administered
CC treat diseases associatly by expressing encoding polynucleotides, to
treat diseases associatly by expressing encoding polynucleotides, to
c treat diseases associated with DNA cytosine methyltransferase, such as
cc neoplastic disorders e.g. carcinomas, sarcomas and leukemias. They can
be used to disganose, or determine susceptibility to neoplastic disorders,
by assaying for polypeptide expression levels in mammalian cells/body
fluids. They are useful to screen for compounds inhibiting/activating the
copolypeptide. The polypeptides can also be used for in vitro de novo
cr methylation of DNA. Such in vitro methylation may be used to direct or
regulate DNA expression in biological systems, e.g. recombinant DNA
condecrase expression of a desired polypeptide for which the native DNA
is under-methylated or not methylated. The polypeptides can also be
colypeptide or therapeutically e.g. to treat neoplastic disorders. The
polypeptide or therapeutically e.g. to treat neoplastic disorders. The
cuseful diagnostically.
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99.7%; Score 4181.4; DB 21; Length 4192;
Best Local Similarity 99.9%; Pred. No. 0;
Marches 4186; Conservative 0; Mismatches 6; Indels 0; C
                                                                                                                                             New mouse and human polypeptides, useful to treat and diagnose neoplastic disorders e.g. carcinomas, sarcomas and leukemias
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                                                                                                                                                                                                                                            Claim 8; Fig 1A; 114pp; English
Okano M, Xie
                                                              WPI; 2000-106298/09
                                                                                        P-PSDB; AAYS4055
Li E,
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8 9	GGTGGGGCCCCAGCTGAAGGGAAACTGAAGCCCCTGCAGAAGCCTCCCGAGAGGCCAAAGAGGCAAAAAACGGAAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAGAGGCCAAAAAA
Db 15 Qy 16 Db 16	561 CCAGCCAAGAAACCCAGAAACAGAAACCAAAAGGTCAAGGTCAAGGAGATCATTGAT 1620 621 GAGCGCACAAAGGAGCGGCTGGTGTATGAGGTGCGCCAGAAGTGCAGAAACATCGAGGAC 1680 621 GAGCGCACAAGGGGGTGTGTATGAGGTGCGCCAGAAGTGCAGAAACATCGAGGAC 1680

1 CTGGAGCTGCAAGAGTGTCTGGAGCACGGCAGAATAGCCAGGATTCAGCA ATTACCACCAGGTCAAACTCTATAAAGCAGGGCAAAGACCAGCATTTCC
ACTTCTGGGGTAACCTTCCTGGCATGAACAGGCCTTTGGC
1 CTTGAGTCTAACCCCGTGATGATTGACGCCAAAGAAGTGTCTGCTG
1 IGGCTCTTTGAGAATGTGGTGGCCATGGGCGTTAGTGACAAGAGGGACATCTCG
AGTTCTACCGCCTCCTGCATGATGCGCGGCCCAAGGAGGAGATGATCGCCCCTTCTT
1 CTCTCCATTGTCAACCCTGCCCGCAAGGGACTTTATGAGGGTACTGGCCGC
1 AAGCATATCCAGGAGTGGGGCCCATTCGACCTGGTGATTGGAGGCAGTC
1 GGCATGGTGCGGCACCAGGGAAAGATCATGTACGTCGGGGACGTCCGCAC
1 CTGGGCATCCAAGTGGACCGCTACATTGCCTCCGACGTGTGTGACGACT-
1 CCCATCCGCGTGCTGTCTCTTTGATGGGATTGCTACAGGGCTCCTGG-
1 CATGACCAGGAATTTGACCCCCCAAAGGTTTACCCACCTGTGCCAGCT
. GGGCTGCTGCGAAGACGGGAAGACTGGCCTTCTCGACTCCAGATGTTCTTTGC
1 CAGGCAGCCATTAAGGAAGACCCCTGGAACTGCTACATGTGCGGGCATAAGGGCA
AACTGCTGCAGGTGCTTTTGTGTCGAGTGTGTGGATCTCTTGGTGGGGC
1 TACCAGTCCTATTGCACCATCTGCTGTGGGGGGGCGTGAAGTGCTCATGT0
1 ATGTGCCAGAACTGTAAGAACTGCTTCTTGGAGTGTGCTTACCAGTATGAC
ATTTGTATCTCATGTGGGAGCCTCAATGTCACCCTGGAGCACCCACTCTTCATTGGAGG

8	Дb	8	망	Ş	В	δ	В	γQ	В	γQ	рь	δ	ర్జ	Q	₽	γ0	뭥	8	Db	δ	90	Ş	рb	Qy	뮍	Qy	뭥	Ş	ф	8	рь	γQ	뭥	γQ	망	Ş
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CAGGATGGGGAGGAGCAGCTGGAGGGGGTTTTAACAAACTGAAGGATGACCCATAT 3900	84	AGGGTTTCAGC	ATATATATAAAAGGTACTGTTAACTACTGTACATCCCGACTTCATAATGGTGCTTTCAAA 3780	GGTGCTTTCAAA 3	GATATGAGATAT 37	GATATGAGATAT 3	AGACACTITCTACAGTATTTCAGGTGCCTACCACACAGGAAACCTTGAAGAAAACCAGTT 3660	AGAAAACCAGTT 36	GAACACCACACC 36	GAACACCACACC 36	CGGAGGCAGAGTCTCCTCCCACCCCCGAGCAGTCTCAA	AGAGACCCTCGGAGGCAGAGTCTCCTCTCTCCCACCCCCGAGCAGTCTCAACAGCACC 35	TATATATCTCTTTGGTTGTCTCTAGCCTGATCAGATAGGAGCACAAA	TTTCTATATATATCTCTTTGGTTGTCTCTAGCCTGATCAGATAGGAGGCACAAACAGGAAGAG 3480	AGAGGGAAAATTCTATAAAAACTTAAAAATATTGGTTTTTTTT	AGAGGGAAAATTCTATAAAAACTTAAAATATTGGTTTTTTTT	;CAGCAAAATCAGTAACAACAAAAAGTAGAAATGCC	CAAGAGAGTTATTGCAGCAAAATCAGTAACAACAAAAAGTAGAAATGCCTTGGAGAG 3	GGGGTTTTC	TTTTTCAGAGGGGTTTTCTGTTTGTTTTGTTTCTTGCTGTC	GCCCCTCCCCTTCTCCCCTCCGGTCCTAGGAGGCGAACTTTTTGTT 3	gcaaaataggcccctccccttcttctccctccggtctaggaggcgaact	TIGGACATCATCTCTGAGTTTTCAATGTTAACCTTCAGTCCTATCTA 3	делаладодсттедасателетествастттелатетталесттелетестатета з	NGGAATTTAAAGCAAACCACAGAGGAGGAAAACGCCGGAGG	SAGAAAAAGGAATTTAAAGCAAACCACAGAGGAGGAGAAAACGCCGGAGGGCTTGGC 31		acgagaggacggagaaaagttcag)GGGCAAACTGAAGTAGTGATAAAAAAGTTAAACAAACAAA	ATGGGGGCAAACTGAAGTAGTGA	GCCACCTCTTCGCTCCGCTGAAGGAATATTTTGC	GGAGCGTGCCGGTCATCCGCCACCTCTTCGCTCCGCTGAAGGAATATTTTGCTTGTT		ACACAGACGTCTCCAACATGAGCCGCTTGGCGAGGCAGAGACTGCTGGGCCGATCG 28		ATCCTGTGGTGCACTGAAATGGAAAGGGTGTTTGGCTTCCCCGT

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The present sequence encodes a human de novo DNA cytosine methyltransferase designated DNMT3A. The polypeptides can be administered therapeutically, especially by expressing encoding polynucleotides, to treat diseases associated with DNA cytosine methyltransferase, such as neoplastic disorders e.g. carcinomas, sarcomas and leukemias. They can be used to disagnose, or determine susceptibility to neoplastic disorders by assaying for polypeptide expression levels in mammalian cells/body
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CACCCCCCACCCCTGCCCCATGCCTAGCTTCACCTGCCAAAAAGGGGCTCAGCTGAGGTG
                  3901 CACCCCCACCCCTGCCCCATGCCTAGCTTCACCTGCCAAAAAGGGGCTCAGCTGAGGTG
                                                                                        GTCGGACCCTGGGGAAGCTGAGTGTGGAATTTATCCAGACTCGCGTGCAATAACCTTAGA
                                                                                                                                                       4021 ATATGAATCTAAAATGACTGCCTCAGAAAATGGCTTGAGAAAACATTGTCCCTGATTTT
                                                                                                                                                                                      GAATTCGTCAGCCACGTTGAAGGCCCCTTGTGGGATCAGAAATATTCCAGAGTGAGGGAA
                                                             GTCGGACCCTGGGGAAGCTGAGTGTGGAATTTATCCAGACTCGCGTGCAATAACCTTAGA
                                                                                                                         ATATGAATCTAAAATGACTGCCTCAGAAAATGGCTTGAGAAAACATTGTCCCTGATTTT
                                                                                                                                                                                                                 4081 GAATTCGTCAGCCACGTTGAAGGCCCCTTGTGGGATCAGAATATTCCAGAGTGAGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "de novo DNA cytosine methyltransferase DNMT3A"
                                                                                                                                                                                                                                               4141 AGTGACCCGCCATTAACCCCNCCTGGAGCAAATAAAAAAACATACAAAATGT 4192
                                                                                                                                                                                                                                                                   4141 AGTGACCCGCCATTAACCCCCNCCTGGAGCAAATAAAAAAACATACAAAATGT 4192
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353..3091
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24-JUL-1998;
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fluids. They are useful to screen for compounds inhibiting/activating the polypeptides can also be used for in vitro de novo methylation of DNA. Such in vitro methylation may be used to direct or regulate DNA expression in vitro methylation may be used to direct or regulate DNA expression in biological systems, e.g. recombinant DNA methylated in vitro may be introduced into a cell/organism to increase or decrease expression of a desired polypetide for which the native DNA is under-methylated or not methylated. The polypeptide can also be used to produce antibodies which are useful to detect and purify the polypeptide or therapeutically e.g. to treat neoplastic disorders. The useful diagnostically.
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68.5%; Score 2871.8; DB 21; Length 4416;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 3574; Conservative 0; Mismatches 583; Indels 113; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4416 BP; 1107 A; 1131 C; 1327 G; 851 T; 0 other;
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2937 TGTGTAAGGGACATGGGGGCAAACTG.	D Q	υ μ
2877 ATCGTGGAGCGTGCCGGTCATCCGCC.	. Оу	N H
	da VQ	1737 AGGCATGTGCCAGAACTGTAAGAACTGCTTCTTGGAGTGCGTTACCAGTATGACGACGA 1796
75	, B &	1677 GGACATTTGTATCTCATGTGGGAGCCTCAATGTCACCCTGGAGCACCCACTCTTCATTGG 1736
S GACCATTACTACGAGGTCAAACTCC S GACCATTACTACGAGGTCAAACTCC) B 5	1617 TGATGAGCGCACAAGGGAGCGGCTGGTGTATGAGGTGCGCCAGAAGTGCAGAAACATCGA 1676
, או) B 6	1557 CCCACCAGCAAGAAACCCAGAAAGAGACACAGAGAAAACCTAAGGTCAAGGAGATCAT 1616
THE TAX OF	B &	1497 TTACAAGGAAGTTTACACCGACATGTGGGTGGAGCCTGAAGCAGCTGCTTACGCCCCACC 1556
	2 d 3	1437 CGGTGGCTTCCAGCCCTCGGGTCCTAAGGGCCTGGAGCCAGCAGAAGAAGAAGAAGAAGACC 1496
05	Q	1377 TGAAAGTGACAGTGGCAAGGCTGTGGAAGTGCAGAACAAGCAGATGATTGAATGGGCCCT 1436
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IGACCICICCAITGICAACCCTGCC) B &	1257 CAGTGCATTCCACCAGGCCACCTACAACAAGCAGCCGTTGTACGGAAAGCCATCTACGA 1316
; 0, -	D	1197 CGGAGATGGCAAGTTCTCAGTGGTGTGTGTGGAGAAGCTCATGCCGCTGAGCTCCTTCTG 1256
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1 01 -	0 2 4	1017 CAAGAATGCTACCAAAGCAGCCGACGATGAGCCTGAGTATGAGGATGGCCCGGGGCTTTGG 1076
2037 TAACCATGACCAGGAATTTGACCCCC	S B S	957 GGACCCTGCTTCTCCGACTGTGGCCACCCCCTGAGCCAGTAGGAGGGGATGCTGGGGA 1016
5 7	da Yo	897 GGCCTCTGGAGAGTCTCAGAAGGTGGAGGAGGCCAGCCCTCCTGCTGCAGCAGCCCAC 956
	Оу	837 AAGGGAGGCTGAGAAGAAAGCCAAGGTAATTGCAGTAATGAATG

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3085 TGTGTAAGGGACATGGGGGCAAACTGAGGTAGCGACACAAAGTTAAACAAAACA	рb
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2817 CGTCCACTACACAGACGTCTCCAACATGAGCCGCTTGGCGAGGCAGAGACTGCTGGGCCG 2876	유 성
905 CATGAATGAGAAAGAGGACATCTTATGGTGCACTGAAATGGAAAGGGTATTTGGTTTCCC 29	D
57 CATGAACGAGAAGGAGACATCCTGTGGTGCACTGAAATGGAAAGGGTGTTTTGGCTTTCCC 28	Ş
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277 ACAGAAGCATATCCAGGAGTGGGGCCCATTCGACCTGGTGATTGGAGGCAGTCCCTGCAA 23	Ş
2217 GETGGCATGGTGCGGCACCAGGGAAAGATCATGTACGTCGGGGACGTCCGCAGCGTCAC 2276	B 6
3GGCATTCAGGTGGACCGCTACATTGCCTCGGAGGTGTGTGAGGACTCCATCA	멍
2157 GGACCTGGGCATCCAAGTGGACCGCTACATTGCCTCCGAGGTGTGTGAGGACTCCATCAC 2216	Q
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidabetic; antifilammatory; antiuleer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancer of the adrenal gland, bone, marrow, breast, gastroincestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic ansemia, autoimmune thyroiditis, diabetes mallitus, Crohn's disease, multiple solerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                       4063 AACATTGTCCCTGATTTTGAATTCGTCAGCCACGTTGAAGGCCCCTTGTGGGATCAGAAA 4122
                                                                        4270 TCTTCAGGCCCAGTTTCTCACTTTAGCCAATTCGAGGCTCCTTGTGGGGATCAGAAC 4329
4210 TAACCCTTTGATTGTTTTCTAAAAGGAGACTCCCTCGGCAAGATGGCAGAGGGTACGGAG 4269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prevention of neural, immine system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders -
                                                                                                                Claim 4; SEQ ID NO 953; 2081pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polynucleotide SEQ ID NO 953.
                                                                                                                                                                                                                                                                                                                                 ABL90391 standard; cDNA; 2938
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                                                                                                                                                                                         TACAAATGT 4192
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P-PSDB; ABB89982.
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QY 2346 CATTGTCAACCCTGCCCGCAAGGGACTTTATGAGGTACTGGCCGCCTCTTTTGAGTT 2405	QY 2286 TATCCAGGAGTGGGGCCCATTCGACCTGGTGATTGGAGGGAG	Qy 2226 GGTGCGGCACCAGGGAAAGATCATGTACGTCGGGGGACGTCCGCAGCGTCACACAGAAGCA 2285	AAGTGGACCGCTACATTGCCTCCGAGGTGTGAGGACTCCATCACGGTGGGCAT 22 	Qy 2106 CCGCGTGCTGTCTCTTTGATGGGATTGCTACAGGGCTCCTGGTGCTGAAGGACCTGGG 2165	e ν H—H	OY 1986 GCTGCGAAGACGGGAAGACTGGCCTTCTCGACTCCAGATGTTCTTTGCCAATAACCATGA 2045	Qy 1926 AGCCATTAAGGAAGACCCCTGGAACTGCTACATGTGCGGGCATAAGGGCACCTATGGGCT 1985	Qy 1866 CTGCAGGTGCTTTTGTGTCGAGTGTGGATCTCTTTGGTGGGGCCAGGAGCTGCTCAGGC 1925	Qy 1806 GTCCTATTGCACCATCTGCTGGGGGGGGGCGTGAAGTGCTCATGTGTGGGAACAACAACTG 1865	QY 1746 CCAGAACTGTAAGAACTGCTTCTTGGAGTGTGCCTTACCAGTATGACGACGATGGGTACCA 1805	TCATGTGGGAGCCTCAATGTCACCCTGGAGCACCCACTCTTCATTV	QY 1626 CACAAGGGAGCGGCTGGTGTATGAGGTGCCCAGAAGTGCAGAAACATCGAGGACATTTG 1685	ត្ត—ត្ត	RETGGGTGGAGCCTGAAGCAGCTGCTTACGCCCCACCCCCCCC	SCCACCAGAAGAAGAGAATCCTTACAAGGA 	Query Match 43.3%; Score 1814; DB 24; Length 2938; Best Local Similarity 82.5%; Pred. No. 0; Matches 2327; Conservative 5; Mismatches 398; Indels 89; Gaps 19;	XX SQ Sequence 2938 BP; 759 A; 695 C; 774 G; 700 T; 10 other;
	Db 1918 GAGGAAAGGTGGGAGAGAGGAAAAAAGGAAATTCTATAGAAATCTATATATA	3299 TGAAACAAGAGAGTTATTGCAGC-AAAATCAGTAACAACAAAAAGTAGAAATGCCTTGGA	QY 3239 TTTTCTACTCTTTTTCAGAGGGGTTTTCTGTTTTGTTTT	OY 3183 AAGCAAAATAGGC-CCCTCCCCTTCTCCCCTCCGGTCCTAGGAGGCGAACTTTTG 3238	QY 3123 TGCAAAAGGGTTGGACATCATCTCCTGAGTTTTCAATGTTAACCTTCAGTCCTATCTAAA 3182	QY 3065 AGAGAAAAAGGAATTTAAAGCAAACCACAGAGGAGGAAAAACGCCGGAGGGCTTGGCCT 3122	3006 1560	2946 1509	2886 COTGCCGGTCATCCGCCACCTCTTCGCTCCCCTGAAGGAATATTTTGCTTGTTGTAAGG 2	2826 CACAGACGTCTCCAACATGAGCCGCTTGGCGAGGGCAGAGACTGCTGGGCCGATCGTGGAG	766 329	CACCAGGTCAAACTCTATAAAGCAGGGCAAAGACCAGCATTTCCCCGTCTTCATGAACGA	QY 2646 GCTGCAAGAGTGTCTGGAGCACGGCAGAATAGCCAAGTTCAGCAAAAGTGAGGACCATTAC 2705	QY 2586 CTGGGGTAACCTTCCTGGCATGAACAGGCCTTTGGCATCCACTGTGAATGATAAGCTGGA 2645	QY 2526 GTCTAACCCCGTGATGATTGACGCCAAAGAAGTGTCTGCTGCACACGGGCCGGTTACTT 2585	2466 CHINGAGAANGIGGIGGCCATGGGCGTTAGTGAGAAGAGGACATCTCGCGATTTCTTGA 2	969 CTACCGCCTCCTGCATGATGCGCGGCCCAAGGAGGAGGATGATCGCCCCCTTCTTCTGGCT

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3494 GGAGGCAG-AGTCTCCTTCCCACCCCCGAGCAGTCTCAACAGCACCATTCCTGGTCAT 3552
                                                                                                                                                                                                                                                                            2335 GGTACTGTTAACTACTGTACAACCCGACTTCATAATGGTGCTTTC-AAACAGCGAGATGA 2393
                                                                                                                                                                                                                                                                                                            3793 GCAAAGACATCAGCTTCCGCCTGGCCCTCTGTGCAAAGGGTTTCAGCCCAGGATGGGGAG 3852
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                    2098 TCAGGGGGCACATTTCCCTCCCAGCCACTGAGCTGTGGTGGCGAGCACCATTCCTGGTCAC
                                                                                                                                                                                                    2634 TIGITITCTAAAAGGAGACTCCCTCGGCAAGATGGCAGAGGTACGGAGTCTTCAGGCCC
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/product= "de novo DNA cytosine methyltransferase
| Dnmt3b1"
                                                                                 2158 GCAAAACAGAACCCAGTTAGCAGCAGGAGACGAGAACACCACAAAAACA-TTTTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2694 AGTITCTCACTITAGCCAATTCGAGGCTCCTTGTGGTGGGATCAGAACTAATCCAGAGT
                                                            DNA encoding de novo DNA cytosine methyltransferase Dnmt3b1.
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269..2848
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The present sequence encodes a murine de novo DNA cytosine
methyltransferase designated Dnmt3b1. The Dnmt3b gene also produces,
through alternate splicing, at least two shorter isoforms of 840 and
control of through alternate splicing, at least two shorter isoforms of 840 and
control of the specification. The polypeptides can be administered
control of given in the specification. The polypeptides can be administered
control of specification. The polypeptides can be administered
control of specification. The polypeptides can be administered
control of specification. The polypeptides can also be used to disagnose, or determine susceptibility to neoplastic disorders,
control of the polypeptide expression levels in mammalian cells/body
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control of DNA. Such in vitro methylation may be used for in vitro and control of control of a desired polypeptide can also be
control of produce antibodies which are useful to detect and purify the
control of produce antibodies which are useful to detect and purify the
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The polypeptide or therapeutically e.g. to treat neoplastic disorders.

The polypeptide or therapeutically e.g. to treat neoplastic disorders.

The polypeptide or therapeutically e.g. to treat neoplastic disorders.

The polypeptide are useful to produce probes and primers which are
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Best Local Similarity 63.4%; Pred. No. 4.7e-174;
Matches 1250; Conservative 0; Mismatches 702; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New mouse and human polypeptides, useful to treat and diagnose neoplastic disorders e.g. carcinomas, sarcomas and leukemias
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                                                                                                                                                               98US-0090906.
                                                                          99WO-US14373
                                                                                                                                                                                                                                                                                             (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-106298/09.
P-PSDB; AAY54056.
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24-JUL-1998;
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AAZ37098 standard; DNA; 4145

27-MAR-2000 (first

DNA encoding de novo DNA cytosine methyltransferase DNMT3B1

carcinoma; sarcoma; leukaemia; DNA methylation; ss. De novo DNA cytosine methyltransferase; DNMT3B1; neoplastic disorder;

sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 17.9%; Score 749.8; DB 21; Length 4145; Best Local Similarity 62.5%; Pred. No. 4.2e-172; Matches 1234; Conservative 0; Mismatches 717; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4145 BP; 1041 A; 1083 C; 1096 G; 925 T; 0 other;
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CCAGGTCAAACTCTATAAAGCAGGGCAAAGACCAGCATTTCCCCCGTCTTCATGAACGAGA 2767
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Query Match Best Local Similarity

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Length

Sequence 709

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163 A; 177 C; 193 G; 168 T; 8 other;

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                                                                               CC ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially creatives of cancer tissues. ABB78993 to ABB79004 represent proteins concerded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be cused in antisense therapy. An antibody immunoreactive with a polypeptide cc encoded by (I) is useful for detecting cancer in a patient sample, and cc nucleic acid which hybridises to (I) in a cell. A probe/primer derived cc from (I) can be used for determining the presence of a nucleic acid which hybridises to (I) in a cell. A probe/primer derived cc hybridises to (I), and for determining the presence of a nucleic acid which cc fells from a patient. (I) is useful for determining the presence of cf cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or cc state of other type of cancer, in antisense therapy, to generate corresponding gene resides, and in tissue profiling, forensics, genetic cantipolies, mapping and diagnostic applications. (I) can be used to raise and to accreen for neartifice analysis, mapping and cancers and antiscness and antiscness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid that is differentially expressed in tissues useful for determining the presence of colon cancer in or tissue type, and in antisense therapy
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Thiaglingam A, Lewis
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9
73; Indels
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens. The colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therewent by the production. N and P may be used in the prevention, chargapy and vaccine production. N and P may be used in the prevention, cassociated with decreased expression by rectifying mutations or deletions associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis to express the proteins and present call and culturing the cell concernment of colorectal carcinomas and cancers. Additioning the cell cand page septent invention.

NB. Pages 66 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
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                                                                                                                                                                       Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
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Best Local Similarity 72.3%; Pred. No. 4.1e-123;
Matches 703; Conservative 4; Mismatches 266; Indels 0;
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                                                                          Rosen CA;
                                                                                                                                                                                                                                  Claim 1; Page 2829; 9803pp; English.
                                                                          Birse CE,
                                    (HUMA-) HUMAN GENOME SCI INC.
99US-0163280.
                                                                            Ruben SM, Barash SC,
                                                                                                                   WPI; 2001-235357/24.
P-PSDB; AAG74429.
03-NOV-1999;
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
Primer sets for synthesizing polynucleotides, particularly the 5602 \, {\rm full}-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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                                                                                                                                                                                                                                                                                                                        Human; primer;
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                                                                                   Isogai T,
Sugiyama
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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T, Wakamatsu
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Otsuki
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XXXOOOOOOOOOOOOOOOOOOOOO Claim 8; SEQ ID 11099; 2537pp + CD ROM; English

sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs against to AAH13628 and AAH13633 to AAH13642 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of represent oligo of the present of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end oligonucleotide comprises at least 15 nucleotides; or (b) a the 5602 nucleotide sequences defined in the specification, invention describes primer sets for synthesising 5602 invention. combination where the

Sequence 3017 BP; 749 A; 751 C; 760 G; 757 T; 0 other;

S S 밁 Ś В Ś 밁 Ś 밁 Ś 밁 Ś 밁 Ş D Ş 묽 Ş 맒 밁 Ş Matches Best Query Match 1617 2157 1797 1737 1677 2097 1977 1917 1857 849 609 489 429 729 669 549 Local GGTGGGCATGGTGCGCACCAGGGAAAGATCATGTACGTCGGGGACGTCCGCAGCGTCAC GGACATTTGTATCTCATGTGGGAGCCTCAATGTCACCCTGGAGCACCCACTCTTCATTGG 1736 TGATGAGCGCACAAGGGAGCGGCTGGTGTATGAGGTGCGCCAGAAGTGCAGAAACATCGA 1676 GAAGCCCATCCGCGTGCTGTCTCTTTGATGGGATTGCTACAGGGCTCCTGGTGCTGAA CTATGGGCTGCTGCGAAGACGGGAAGACTGGCCTTCTCGACTCTCCAGATGTTCTTTGCCAA 2036 GGACCTGGGCATCCAAGTGGACCGCTACATTGCCTCCGAGGTGTGTGAGGACTCCATCAC GGGGCTCTGTCAGACATGCCGGGATCGCTTCCTTGAGCTGTTTTACATGTATGATGACGA AGGCATGTGCCAGAACTGTAAGAACTGCTTCTTGGAGTGTGCTTACCAGTATGACGACGA 1796 AGATEGCTGTTTGTCGCAGGAAAAACCCCGTGTCCTTCCACCCTCTCTTTGAGGG TGAAGATCAGAGCCGAGAACAAATGGCTTCAGATGTTGCCAACAACAAGAGCAGCCTGGA 488 GCGGCCCATTCGAGTCCTGTCATTGTTTGATGGCATCGCGACAGGCTACCTAGTCCTCAA TGGCACGGGGCTTGAATACGAAGCCCCCAAGCTGTACCCTGCCATACCCGCAGCCCGAAG TAACCATGACCAGGAATTTGACCCCCCAAAGGTTTACCCACCTGTGCCAGCTGAGAAGAG TCATGGCGTCCTGCGGCGCCGGAAGGACTGGAACGTGCGCCTGCAGGCCTTCTTCACCAG AGCGGCCGAGGCCAAGCTTCAGGAGCCCTGGAGCTGCTACATGTGTCTCCCGCAGCGCTG TGCTCAGGCAGCCATTAAGGAAGACCCCTGGAACTGCTACATGTGCGGGCATAAGGGCAC 1976 CACGAGCTGCTGCCGGTGTTTCTGTGTGGAGTGCCTGGAGGTGCTGGTGGGCACAGGCAC 728 CAACAACTGCTGCAGGTGCTTTTGTGTCGAGTGTGTGGATCTCTTGGTGGGGGCCAGGAGC 1916 TGGCTATCAGTCTTACTGCACTGTGTGCTGCGAGGGCCGAGAGCTGCTGCTTTGCAGCAA TGGGTACCAGTCCTATTGCACCATCTGCTGTGGGGGGCGTGAAGTGCTCATGTGTGGGAA 1856 685; Similarity Conservative 11.5%; 67.0%; <u>.</u> Score Pred. Mismatches 482.8; DB 22 No. 4.5e-107; 337; 22; Indels Length 3017; 0 Gaps 2276 2156 848 2216 896 668 608 548 806 2096 788 0

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2000US - 0234294
2000US - 0234994
2000US - 0234999
2000US - 0235834
2000US - 0235834
2000US - 0235834
2000US - 0235836
2000US - 0236363
2000US - 02340960
2000US - 02340960
2000US - 02340960
2000US - 02411785
2000US - 02411785
2000US - 02411785
2000US - 02411786
2000US - 02411786
2000US - 02411869
  Human; reproductive system related antigen; reproductive system disorder;
cancer; gene therapy; ss.
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1209 CTTCGAATTTTACCACCTGCTGAATTACTCACGCCCCAAGGAGGGGGGAGATGACCGGCCGTT
                                                                                                                                                                                                                                                                                                                                                                        CTTCTGGCTCTTTGAGAATGTGGCCATGGGCGTTAGTGACAAGAGGGGACATCTCGCG
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                                                                          2277 ACAGAAGCATATCCAGGAGTGGGCCCCATTCGACCTGGTGATTGGAGGCAGTCCCTGCAA
                                                                                                       1089 AAAGAAAATATGAAGAATGGGGCCCATTTGACTTGGTGATTGGCGAAGCCCATGCAA
                                                                                                                                                                                                                                                                         CTTTGAGTTCTACCGCCTCCTGCATGATGCGCGGCCCAAGGAGGAGGAGATGATCGCCCCTT
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2000US-0180628.
2000US-018663.
2000US-018974.
2000US-019076.
2000US-0190176.
2000US-0209467.
2000US-0217487.
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Best Local Similarity
Matches 471; Conserv
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17-NO
                                                                                      1446
                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a coding sequence of the
1506 AGTTTACACCGACATGTGGGTGGAGCCTGAAGCAGCTGCTTACGCCCCACCCCCACCAGC 1565
                                                                                                                                                                                                                   Sequence 622
                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN
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                                                                    CCAGCCCTCGGGTCCTAAGGGCCTGGAGCCACCAGAAGAAGAAGAAGAATCCTTACAAGGA 1505
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                                         CCAGCCTTCTGGCCCTAAGGGCCTAGAGCCACCAGAAGAAGAAGAATCCCTACAAAGA
                                                                                                                                                                                                                                                                                                                                                                              1; SEQ ID NO 272; 1297pp + Sequence Listing; English.
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2000US-0246524.
2000US-0246526.
2000US-0246528.
2000US-0246611.
2000US-0246611.
2000US-0249209.
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2000US-0251869.
2000US-0251989.
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2000US-0251999.
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                                                                                                                                Conservative
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                                                                                                                                                9.9%;
                                                                                                                                                                                                               A; 161 C; 189 G; 112 T; 6 other;
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                                                                                                                            Score 413; DB 22;
Pred. No. 2.1e-90;
2; Mismatches 62;
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RESULT 10
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome

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and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical isorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in claspnostics, forensics, gene mapping, identification of mutations in capponable for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences. AASA94564 represent movel human caid sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO. It fip.wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2170 CAAGTGGACCGCTACATTGCCTCCGAGGTGTGTGAGGACTCCATCAGGGTGGGCATGGTG 2229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2230 CGGCACCAGGGAAAGATCATGTACGTCGGGGACGTCCGCAGCGTCACACAGAAGCATATC 2289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2530 AACCCCGTGATGATTGACGCCAAAGAAGTGTCTGCTGCACAGGGCCCGTTACTTCTGG 2589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 CACCTGCTGAATTACTCACGCCCCAAGGAGGGTGATGACGGCCGGTCTTCTGGATGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2410 CGCCTCCTGCATGATGCGCGGCCCAAGGAGGAGGATGATCGCCCCTTCTTCTGGCTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2470 GAGAATGTGGTGGCCATGGGCGTTAGTGACAAGAGGGACATCTCGCGATTTCTTGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 GAGAATGTTGTAGCCATGAAGGTTGGCGACAAGAGGGACATCTCACGGTTCCTGGAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.1%; Score 341; DB 23; Length 711;
74.7%; Pred. No. 7.9e-73;
ve 0; Mismatches 145; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 711 BP; 181 A; 164 C; 199 G; 167 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2650 CAAGAGTGTCTGGAGCACGCCAGAATAGCCAAG 2682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF80537 standard; cDNA; 2077 BP
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Matches 428; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUN-2001
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The present invention relates to a composition comprising several polynucleotide probes. Probes can be derived from the present sequence. The probes are immobilised and are preferably useful as hybridisable array elements in a microarray for monitoring the expression of several carray elements in a microarray can be used in the diagnosis of cancers uch as adenocarcinoma, leukasmia, lymphoma, melanoma, myeloma, sarcoma and terratocarcinoma etc., immunopathology such as Albs, Addison's disease, adult respiratory distress syndrome, allergies, anaemia, asthma, atherosclerosis and bronchitise etc., neuropathology such as Alzheimer's disease, ammesia, amyotrophic lateral sclerosis, bipolar disorder, caratomia and cerebral neoplasms etc. The microarray can also be used to investigate an individual's predisposition to a disease such as cancer, immunopathology or neuropathology. Also, the microarray can be used for investigating cellular response to infection, drug treatment etc. The microarray can be used for diagnostics, prognostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, forensics, pharmacogenomics etc. The array can also be used for monitoring disease progression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition having probes which comprise part of gene sequence encoding proteins associated with cell proliferation useful as hybridizable array elements in Microarrays to monitor expression of target polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2387 GCCGCCTCTTTTGAGTTCTACCGCCTCCTGCATGCGCGGCCCCAAGGAGGAGAGTG 2446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 2077;
                                                             Probe; microarray; cancer; immunopathology; neuropathology; ss
                                                                                                                                                                                                                                                                                                                                                                          Guegler KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.7%; Score 324.6; DB 22; Length
14.8%; Pred. No. 1.4e-68;
ve 0; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2077 BP; 539 A; 485 C; 477 G; 567 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                       Yue H, Reddy R,
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                Receptor #25 partial coding sequence.
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Best Local Similarity
                                                                                                        Balaena mysticetus.
                                                                                                                                                                                                                                         25-MAR-1999;
                                                                                                                                                                                                                                                                                    27-MAR-1998;
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Baughn MR;
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RESULT 12
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         A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDMAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be appearance frequency of a given GS in a cDNA library can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                     Identifying gene signatures in 3'-directed human cDNA library - for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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(esp. using primers
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                                                                                                                                                                                                                         2245pp; Japanese
 and probes derived from
   the GS
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                     11-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
11-APR-2000;
11-APR-2000;
11-APR-2000;
11-APR-2000;
107-JUN-2000;
28-JUN-2000;
30-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirhaumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallargic; antidiabetic; antiucer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds
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2000US-0186350.

2000US-019974.

2000US-0190076.

2000US-0198123.

2000US-0205515.

2000US-020467.

2000US-0214886.

2000US-021613.

2000US-0216647.

2000US-0216647.
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Pred. No. 3.9
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20 - CCT - 2000 j. 2000US - 0244617 08 - NOV - 2000 j. 2000US - 0244417 08 - NOV - 2000 j. 2000US - 0246474 08 - NOV - 2000 j. 2000US - 0246474 08 - NOV - 2000 j. 2000US - 0246524 08 - NOV - 2000 j. 2000US - 0246524 08 - NOV - 2000 j. 2000US - 0246524 08 - NOV - 2000 j. 2000US - 0246526 08 - NOV - 2000 j. 2000US - 0246527 08 - NOV - 2000 j. 2000US - 0246527 08 - NOV - 2000 j. 2000US - 0246527 08 - NOV - 2000 j. 2000US - 0246527 17 - NOV - 2000 j. 2000US - 0249210 17 - NOV - 2000 j. 2000US - 0249211 17 - NOV - 2000 j. 2000US - 0249214 17 - NOV - 2000 j. 2000US - 024924 17 - NOV - 2000 j. 2000US - 024926 17 - NOV - 2000 j. 2000US - 025926 08 - DEC - 2000 j. 2000US - 0251986 08 - DEC - 2000 j. 2000US - 0251986 08 - DEC - 2000 j. 2000US - 0251986 08 - DEC - 2000 j. 2000US - 0251980 08 - DEC - 2000 j. 2000US - 0251980 08 - DEC - 2000 j. 2000US - 0251980 08 - DEC - 2000 j. 2000US - 0251980	(HUMA-) HUMAN GENOME SCI INC. Rosen CA, Barash SC, Ruben SM; WPI; 2001-541565/60.	Nucleic acids encoding 3224 human ner useful for preventing, diagnosing and cancers and metastases - Disclosure; SEQ ID NO 12586; 1701pp +	The invention relates to novel genes (ABB14678-ABB1801) useful for preven medical conditions e.g. by protein or isolated from a range of human tissue The mucleic acids, proteins, antibodi in the diagnosis, treatment and preve and ovarian cancer and other cancers marrow, breast, gastrointestinal trac (b) immune disorders e.g. Addison's c haemolytic anaemia, autoimmune thyroi
\$\times\$\	AX TX B	X T T T X S X	88888888888

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases \dot{z}

Disclosure; SEQ ID NO 12586; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adremal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's

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RESULT 1
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Best Local
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Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease, colitis;
                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                       31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                           11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel
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                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                    uman; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
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21970; 103pp; English
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81.7%;
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Pred. No. 1.0
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TCGAGGACATTTGTATCTCATGTGGGAGCCTCAATGTCACCCTGGAGCACCCCACTCTTCA 1732

TCAGAGCCGAGGTGATTGTTGGGTACCTGGGATCATGGGACAGATGGGAGGAGGACGCTG TCATTGATGAGCGCACAAGGGAGCGGCTGGTGTATGAGGTGCGCCAGAAGTGCAGAAACA 1672

1610

1663

TGCCTTGTCTGAGACATGCCGGGTAAGTCCTCCTACTACTGCCCTGGACCTTCCTCC-TTGGAGGCATGTGCCAGAACTGTAAGAACTGCTTCTTGGAGTGTGCTTACCAGTATGACG

1792

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1496

GAGTCC-----GCCTCAAGACAAATTGCTATAACAACGGCAAAGACCGAGGGGATGAAGA CACCCCCACCAGCCAAGAAACCCCAGAAAGAGCACAACAGAGAAACCTAAGGTCAAGGAGA 1612

1550

1613

1436 1493

ATCCTTACAAGGAAGTTTACACCGACATGTGGGTGGAGCCTGAAGCAGCTGCTTACGCCC

GTGGGAATGAGTCCCCATGGCAGCACCCGCTGCCTCTGCTGGTGGGACCACTTCTTGGGA 1495

1433

AGGGATGAAGCAAGAACCCACAGAATTGGAGGACCAGCTGAAGCCCCATGTTGGAGTGGG

1375

GTGATGAAAGTGACAGTGGCAAGGCTGTGGAAGTGCAGAACAAGCAGATGATTGAATGGG 1432

CCCACGGGGGCTTCAAGCCCACTGGGATCGAGGGCCTCAAACCCCAACAACACGCAACCAG 1435

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cc (II). (II) is useful for generating antibodies against it, detecting or cc quantitating a polypeptide in tissue, as molecular weight markers and as cc a food supplement. (II) and its binding partners are useful in medical cc imaging of sites expressing (II). (I) and (II) are useful in medical cc imaging of sites expressing (II). (I) and (II) are useful for treating cc disorders involving aberrant protein expression or biological activity. Cc The polypeptide and polynucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cc responsible for genetic disorders or other traits to assess biodiversity can to produce other types of data and products dependent on DNA and cc amino acid sequences. AAS64197-AAS94564 represent novel human cc diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO cc at ftp.wipo.int/pub/published pct sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II) The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                  TTGTGTCTTGGTGGATGACAGGCCGGAGCCGAGCAGCTGAAGGCACTCGCTGGGTCATGT 1192
                                                                                                     CTGAGGCTGTGCCTGCCTCCCTTTGAATAAGCTCGTCTCCTATCGAAAAGCCATGT
                                                                                                                                                                                                          GGTTTGGCGATGGCAAGTTCTCCGAGGTGAGTCCGGGGAAGGGGCAAGGGGTTCTGCAGGC 1201
                                                                                                                                                                                                                                                             GGTTCGGAGATGGCAAGTTCTCAGTGGTGGTGTGGAGAAGCTCATGCCGCTGAGCTCCT 1252
ACCATGCTCTGGAGGT-----AACATGGGATGAGGGAATGAGGGCTAAGCCCTGAGAGC 1315
                                                                                                                                                       TCTGCAGTGCATTCCACCAGGCCACCTACAACAAGCAGCCCATGTACCGCAAAGCCATCT 1312
                                                                                                                                                                                                                                                                                                               TGGTGTCTTGGAAGGCCACCTCCAAGCGACAGGCTATGTCTGGCATGCGGTGGGTCCAGT 1141
                                                  ACGAAGICCTCCAGGIGGCCAGCAGCCGIGCCGGGAAGCTGITTCCAGCIIGCCAIGACA 1372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2501 ACAGCCAGGCAGGAAAGCGCTGCTGGCAGTGACAACCTACCCGGGATGAACAGGTAAC 2560
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1722 - cerrideciretrenacirecererierirecirideaddecidaddecideirgeiridea 1780
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                                                                          1853 GGAACAACACTGCTGCAGGTGCTTTTGTGTGGAGTGTGTGGATCTCTTGGTGGGGGCCAG
                                                                                                                                                1913 GAGCTGCTCAGGCAGCCATTAAGGAAGACCCCTGGAACTGCTACATGTGCGGGCATAAGG
                                                                                                                                                                                     1841 AAGGCTCCTACGTTCCTGCAGTCTAGGAGCCCTGGAGCTGTTACATGTGTCTCCCGCAGC
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianemic; antiarthritic; cancer; antitheumatic; hepatocropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune discorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.
2801 GACATGGGCTGCTGGGAAGGTCCTGGAGCGTGCTCTTCTCGACACCTCTTCGCCCCTC 2860
                                                                                                                                                                                               Human nervous system related polynucleotide SEQ ID NO 2738
                                    2918 TGAAGGAATATTTTGCTTGTGTA 2942
                                                        2861 TGAAGGACTACTTTGCATGTGAATA 2885
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2000US-0186564.
2000US-01863564.
2000US-01863564.
2000US-0199076.
2000US-0199123.
2000US-0209467.
2000US-0216886.
2000US-0216886.
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2000US-0216886.
2000US-0216880.
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2000US-0225759.
2000US-0226279.
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                                                                                                                                                                                                                                                                                                                                             WO200159063-A2.
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16-MAR-2000; 2

18-APR-2000; 2

19-MAR-2000; 2

19-MAR-2000; 2

28-JUN-2000; 2

28-JUN-2000; 2

20-JUL-2000; 2

11-JUL-2000; 2

26-JUL-2000; 2

14-AUG-2000; 2
                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                ABA13731;
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08-SEP-2000 08-SEP-2000 08-SEP-2000; 08-SEP-2000;

2000US-0232080.

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01-SEP-2000; 05-SEP-2000; 05-SEP-2000; 06-SEP-2000; 06-SEP-2000;

2000US-0229345. 2000US-0229509.

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17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                               disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia an epilepsy; and (f) infectious diseases such as viral, bacterial, fung and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune theoryticiatis, diabetes mellitus, Crohn's disease, allergies, autoimmune theorytic anaemia, autoimmune theoryticiatis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 3224 human useful for preventing, diagnosing cancers and metastases -
                                                                                                                                                                                                                        Sequence 283
                                                                                                                                                                                                                                                                 Note: The sequence data printed specification, k
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P-PSDB; ABB17405.
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AATGGAGACTTGGAGAAGCGGAGTGAACCCCAACCTGAGGAGGGGGAGCCCAGCTGCAGGG
                                       GCGGTGATCTCCAAGTCCCATCCATGCGCACGAGCTCAGGAGCTATTACCC
                                                                     GCAGTGACCACCAAGTCTCAGCCCATGGCCCAGGACTCTGGCCCCTCAGATCTGCTACCC
                                                                                                                                 AGGCCTGGCCGGAAGCGCAAGCACCCACCGGTGGAAAGCAGTGACACCCCCAAGGACCCA 414
                                                                                                       ATGGCAGGCCCGGCCCTCTGGGTGACCAAGGTGGAAAGCGGTGACACGCCAAAGGACCCT
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2000US-0249265.

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                                                                                                                                                               Conservative
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2000US-0249216.
2000US-0249217.
2000US-0249218.
                                                                                                                                                                                                                        BP; 69
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                                                                                                                                                                            4.0%;
79.8%;
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                                                                                                                                                      Score 167; UB 2
Pred. No. 1.3e-3
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141 AATGGGGACTTGGAGAAGCGGAGTGAGCCCCAGCCAGAGGGGGAGCCCTGCTGGGGGG 200
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Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 4195)
Okano, M. Xie, S. and Li, E.
Cloning and characterization of a family
(cytosine-5) methyltransferases
Nat. Genet. 19 (3), 219-220 (1998)
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Sequence update by submitter
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Location/Qualifiers
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Direct Submission
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LTRETKDTRTRSESPAVRTRHSNGTSSLERQRASPRITRGRQGRHHVQEYPVEFPATR
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EGQIKYVNDVRKITKKNIEBWGPFDLVIGGSPCNDLSNVNPARKGLYEGTGRLFFEFV
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                                                                                                                                                                                                                                                                                                                                                                              /product="DNA cytosine-5 methyltransferase
/protein_id="AAC40178.2"
/db_xref="GI:6449470"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="alternatively spliced product; contains Cys-rich region; C-terminal region is similar to corresponding region of DNA cytosine-5 methyltransferase 3A"
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Accession Numbers AA116694, AA119979, AA177277, AA210568,
AA407106, and AA575617"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="de novo DNA methylation"
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Alignment

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2.1e-249 4590.00 100.00% 100.00% 100.00% 100.00% Matches: Conservative: Indels: Mismatches: 4195 859 0 0 0

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Query Match: US-09-720-086-6 (1-859) x AF068626 (1-4195) Score: á 5 뭐 S 멼 á 밁 Pred. No.: á g Ś 멅 á В Ş 밁 В Ş 8 Ş 밁 Ó 5 밁 Ś S 밁 á 맑 S 밁 밁 269 389 329 1049 1109 689 629 569 509 449 101 749 161 141 121 608 181 301 281 261 989 241 929 221 869 201 81 61 41 21 1 MetLysGlyAspSerArgHisLeuAsnGluGluGluGlyAlaSerGlyTyrGluGluCys CCAGTCTTGGAGGCAATCTGCACAGAGCCAGTCTGCACACAGAGACCAGAGGCCGCAGG ATGAAGGGAGACAGCAGACATCTGAATGAAGAAGAGGGTGCCAGCGGGTATGAGGAGTGC SerSerRerArgLeuSerLysArgGluValSerSerLeuLeuAsnTyrThrGlnAspMet ProValLeuGluAlaIleCysThrGluProValCysThrProGluThrArgGlyArgArg ACCCGACATAGCAATGGGACCTCCAGCTTGGAGAGGCCAAAGAGCCTCCCCCAGAATCACC ProLysLeuThrArgGluThrLysAspThrArgThrArgSerGluSerProAlaValArg ThrGlyAspGlyAspArgAspAspGluValAspAspGlyAsnGlySerAspIleLeuMet TCAAGCTCCCGGCTGTCTAAGAGGGAAGGTCTCCAGCCTTCTGAATTACACGCAGGACATG SerArgArgArgArgAlaSerSerSerAlaSerThrProTrpSerSerProAlaSerVal CGAGGTCGGCAGGGCCACCATGTGCAGGAGTACCCTGTGGAGTTTCCCGGCTACCAGG ArgGlyArgGlnGlyArgHisHisValGlnGluTyrProValGluPheProAlaThrArg ThrArgHisSerAsnGlyThrSerSerLeuGluArgGlnArgAlaSerProArgIleThr 140 CCANAGETTCACCCGTGAGACCAAGGAGACCAGGACGCGCTCTGAAAAGCCCGGCTGTCCGA ACAGGAGATGGAGACAGAGATGATGAAGTAGATGGGGAATGGCTCTGATATTCTAATG GACTTCATGGAAGAAGTGACACCTAAGAGCGTCAGTACCCCATCAGTTGACTTGAGCCAG decardecedaardecendeeracadreeringendardecaacrititereagatete AlaMetProGlyMetArgTrpValGlnTrpPheGlyAspGlyLysPheSerGluIleSer 280 AAGGCTTCTCCTGGTGGCCTGCCATGGTGGTGTCCTGGAAAGCCACCTCCAAGCGACAG AGCACAGAGTATCAGGATGATAAAGAGTTTGGAATAGGTGACCTCGTGTGGGGAAAGATC SerThrGluTyrGlnAspAspLysGluPheGlyIleGlyAspLeuValTrpGlyLysIle AspPheMetGluGluValThrProLysSerValSerThrProSerValAspLeuSerGln AlaAspLysLeuValAlaLeuGlyLeuPheSerGlnHisPheAsnLeuAlaThrPheAsn

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519	mus	35071 Huma	4832 Homo	J404467 Mus musc	AF220524 Mus 1	002560 Homo	194032 Homo	128509 Ratt	22356 Mus	833803 Mus mus	29189 Sequen	29269 Homo s	29268 Homo s	129267 Homo s	09474 Homo s	18214 Homo	07644 Mus	11734 Rat	20824 Rattus	586 Rattus n	25230 Homo s	38 Danic	C007466 Mus mus	068625 Mus mus	6 Homo s	67972 Homo s	01191 Homo s	6487 Homo s	76228 Homo	31857 Homo sap	56488 Homo sapi	F151971 Mus mus	F151976 Mus mus	FORBACAR MILE MILE	151972 Mus musc	F151975 Mus musc	Y078427 Mus musc	51970 Mus mus	Mus mus	Ø	69 Mus musc	s mus	068626 Mus mus		3	

ALIGNMENTS

RESULT 1

Pred. No.:

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AF068626 4195 bp mRNA linear ROD 06-DEC-1999
Mus musculus DNA cytosine-5 methyltransferase 381 (Dnmt3b) mRNA,
alternatively spliced, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xie,S., Okano,M. and Li,E.
Xie,S., Okano,M. and Li,E.
Direct Submission
Submitted (28-MAX-1998) CVRC, Mass. Gen. Hospital, 149 13th Street,
Charlestown, MA 02129, USA
3 (bases 1 to 4195)
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| .4195
|/gene="Dnmt.1b"
| Anote="similar to EST sequences deposited in GenBank
| Accession Numbers AA116694, AA119979, AA17277, AA210568,
| AA407106, and AA575617"
                                                                                                                                                                                                                                                     Mus musculus.

Mus musculus.

Mus musculus.

Mus musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (basea 1 to 4195)

Okano, M., Xie, S. and Li, E.

Cloning and characterization of a family of novel mammalian DNA (cytosine-5) methyltransferases

Mat. Genet. 19 (3), 219-220 (1998)

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/function="de novo DNA methylation"
/function="de novo DNA methylation"
/note="alcernatively spliced product; contains Cys-rich
region; C-terminal region is similar to corresponding
region of DNA cytosine-5 methyltransferase 3A"
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/organism="Mus musculus"
/db_xref="taxon:10090"
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                                            SerAsnValAsnProAlaArgLysGlyLeuTyrGluGlyThrGlyArgLeuPhePheGlu
                                                                                             AsnIleGluGluTrpGlyProPheAspLeuValIleGlyGlySerProCysAsnAspLeu
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Direct Submission
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                                                                                ProValLeuGluAlaIleCysThrGluProValCysThrProGluThrArgGlyArgArg
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                                                              CCAGTCTTGGAGGCAATCTGCACAGAGCCAGTCTGCACACCAGAGACCAGAGGCCGCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J. Shen, Y. Cloning of full-length Dnmt3b cDNA
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DSAASESPPEKLKTNSYGGKDRGEDEESRERMASEVTNNKGNLEDRCLSCGKKNPVS

FHPLFEGGLCQSCRDRFLELFYMYDEDGYQSYCTYCCEGRELLCSNTSCCRCFCVEC
LEVLVGAGTAEDAKLQEPWSCYMCLPQRCHGVLRRRKDWNMRLQDFFTTDPDLEEFEP

PKLYPAIPAKRRPIRVLSLFPGGIATGYLVKEKIGIKVEKYIASEVCAESIAVGTVKH

EGQIKYVNDVRKITKKNIEEMGPFDLVIGGSPCNDLSNVNPARKGLYEGTGRLFFEFY

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FMGNLPGMRRPVMASKNDKLBLQDCLEFSRTAKLKVOTITTKSNSIRQGKPGVVV

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652	 rrctaatg 71
101	ProlysleuThrargGluThrlysAspThrArgThrArgSerGluSerProAlaValArg 120
121	rgilethr 14 GAATCACC 83
141 832	luPheProAlaThrArg 16 GTTTCCGGCTACCAGG 89
161 892	rgargargargalaserserseralaserthrprotrpserserproalaserval 18
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241	LysglypheserTrpTrpProhlaMetValValSerTrpLysAlaThrSerLysArgGln 260
261 192	
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341	8Lys 36
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381	9ArgArgThrThrAsnAspSerAlaAlaSerGluSerPro 40
401	rasnsertyrglyglylysaspargglyC
421	SerargGluargMetAlaSerGluValThrAsnAsnLysGlyAsnLeuGluAspArgCys 440

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4135 bp mRNA linds musculus DNA cytosine-5 methyltransferase Attacheratively spliced, complete cds.
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Okano, M., Xie, S. and Li, E.
Cloning and characterization of
Clytosine-5) methyltransferases
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Direct Submission
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Mammalia; Eutheria;
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SRRRRASSSASTPWSSPASVDFMEEVTPKSVSTPSVDLSQDGDQEGMDTTQVDAESRD
GDSTEYQDDKEFGIGDLVWGKIKGFSWWPAMVVSWKATSKRQAMPGMRWVQWFGDGKF
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                                                                    /codon_start=1
/product="DNA cytosine-5
/protein_id="AAC40179.2"
/db_xref="GI:6449472"
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                                                                                                                                                           /gene="Dnmt3b"
/function="de novo DNA methylation"
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FYMYDEDGYQSYCTVCCEGRELLLCSNTSCCRCFCVECLEVLVGAGTAEDAKLQEPWS
CYMCLPGACHGVLLRRKDWMRLQDFFTTDPDLEEFEFEPKLYPA I FAAKRR PI RVLSL
FDGIARGYLVLKELIGI KVEKY I ASEVCARSI AVGTTVEHEGGI KYVUNDYRKI TEKNI EE
WGPFDLVIGGSPCNDLSNVNPARKGLYEGTGRLFFEFYHLLNYTR PKEGDNR PFFWMF
ENVVANKVNDKKD I SRFLACURVMI DA IKVSAAHRARY FWGNLFGNNR PVMAS KNDKL
ELQDCLEFSRTAKLKKVQTITTKSNS I RQGKNQLFARY YMGKDDVLWCTELER I FGFP
AHYTDVSNMGRGAROKLLGRSWSVPVIRHLFAPLKDY FACE"
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Percent Similarity: US-09-720-086-6 (1-859) ThrGlyAspGlyAspArgAspAspGluValAspAspGlyAsnGlySerAspIleLeuMet MetLysGlyAspSerArgHisLeuAsnGluGluGluGlyAlaSerGlyTyrGluGluCys SerArgArgArgAlaSerSerSerAlaSerThrProTrpSerSerProAlaSerVal SerThrGluTyrGlnAspAspLysGluPheGlyIleGlyAspLeuValTrpGlyLysIle AspPheMetGluGluValThrProLysSerValSerThrProSerValAspLeuSerGln ACCCGACATAGCAATGGGACCTCCAGCTTGGAGAGGCCAAAGAGCCTCCCCCAGAATCACC ThrArgHisSerAsnGlyThrSerSerLeuGluArgGlnArgAlaSerProArgIleThr SerSerSerArgLeuSerLysArgGluValSerSerLeuLeuAsnTyrThrGlnAspMet CCAGTCTTGGAGGCAATCTGCACAGAGCCAGTCTGCACACAGAGACCAGAGGCCGCAGG ProValLeuGluAlaIleCysThrGluProValCysThrProGluThrArgGlyArgArg IleIleValAsnGlyAsnPheSerAspGlnSerSerAspThrLysAspAlaProSerPro Scores: LysGlyPheSerTrpTrpProAlaMetValValSerTrpLysAlaThrSerLysArgGln AspGlyAspGlnGluGlyMetAspThrThrGlnValAspAlaGluSerArgAspGlyAsp GACTTCATGGAAGAAGTGACCTAAGAGCGTCAGTACCCCCATCAGTTGACTTGAGCCAG ArgGlyArgGlnGlyArgHisHisValGlnGluTyrProValGluPheProAlaThrArg CCAAAGCTCACCCGTGAGACCAAGGACACCAGGACGCGCTCTGAAAGCCCGGCTGTCCGA ProLysLeuThrArgGluThrLysAspThrArgThrArgSerGluSerProAlaValArg TCAAGCTCCCGGCTGTCTAAGAGGGGAGGTCTCCAGCCTTCTGAATTACACGCAGGACATG ATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACACGAAGGATGCTCCCTCACCC ATGAAGGGAGACAGCAGACATCTGAATGAAGAAGAGGGTGCCAGCGGGTATGAGGAGTGC AAGGGCTTCTCCTGGTGGCCTGCCATGGTGGTGTCCTGGAAAGCCACCTCCAAGCGACAG GATGGAGATCAGGAGGGTATGGATACCACACAGGTGGATGCAGAGAGCAGAGATGGAGAC TCTCGGAGACGTCGAGCATCGTCTTCAGCAAGCACGCCATGGTCATCCCCTGCCAGCGTC CGAGGTCGGCAGGGCCACCATGTGCAGGAGTACCCTGTGGAGTTTCCGGCTACCAGG Similarity: 9.09e-243 4472.00 97.67% 97.67% 97.43% x AF068627 (1-4135)Mismatches: Indels: Gaps: Length: Matches: Conservative: 4135 839 0 0 20 **FGGGGAAAGATC** 180 1048 62B 100 260 120 448 40 328 986 240 928 220 868 200 808 748 160 889 140 568 508 80 60 386

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AF151974 4163 bp mRNA linear ROD 08-JUN-2000 Mus musculus DNA cytosine-specific methyltransferase isoform 6 (Dnmt3b) mRNA, complete cds.
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Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
P.R.China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 4163)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cloning of full-length Dnmt3b cDNA and its alternative splicing isoforms in mouse embryonic tissue Unpublished 2 (Dases 1 to 4163)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
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2069 ACTGTTAAGCATGAAGGCCAGATCAATATGTCAATGACGTCCGGAAAATCACCCAGAAA 2128
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2429 TTCTGGGGTAACCTACCCGGAATGAACAGGCCCGTGATGGCTTCAAAGAATGATAAGCTC 2488
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                                       ThrArgHisSerAsnGlyThrSerSerLeuGluArgGlnArgAlaSerProArgIleThr
                                                                                                                                              ACAGGAGATGGAGACAGATGATGATGATGATGGGAATGGCTCTGATATTCTAATG
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                    ACCCGACATAGCAATGGGACCTCCAGCTTGGAGAGGCAAAGAGCCTCCCCCAGAATCACC
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QLKPMLEWAHGGFKPTGIEGLKPNKKQPENKSRRRTTNDSAASESPPKRLKTNSYGG
QLKPMLEWAHGGFKPTGIEGLKPNKKQPENKSRRRTTNDSAASESPPKRLKTNSYGG
KDRGEDEESRERMASEVTNNKGNLEDRCLSCGKKNPVSFPLFEGGLCQSCRDRFLEL
FYMYDEDGYQSYCTVCCEGRELLLCSNTSCCCCFFCYECLEVLVGAGTAEDAKLQEPMS
CYMCLPQRCHGVLRRRKOMMRLQDFFTTDPDLEEFEPPKLYPAIPAAKRRPIRVLSL
FDGIATGYLVLKELGIKVEKYIASEVCAESIAVGTVKHEGQIKYVNDVRKITKKNIEE
MGPFDLVIGGSPCNDLSNVNPARKGLYEGTGRLFPEFYHLLNYTRPKEGDNRPFFMMF
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LTRETKDTRTRSESPAVRTRHSNGTSSLERQRASPRITRGRQGRHHVQEYPVEFPATR
SRRRRASSSASTPWSSPASVDFMEEVTPKSVSTPSVDLSQDGDQEGMDTTQVDAESIY
GDSTEYQDDKEFGIGDLVMGKIKGFSWWPAMVVSWKATSKRQAMPGMRWVQWFGDGKF
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AICTEPVCTPETRGRRSSSRILSKRRYSSLLNYTODMTGDCDRDBUDDGNGSDILMPK
LTRETKOTRTRESSPAVRTRHSNGTSSLERQRASPRITRGRQGRHHVQEYPVEFPATP
SRRRAASSSASTPRNSSPAVDFMEEVTPKSVSTPSVDLGODGDGGCHUTTQVDAESI
GDSTEYQDDKEFGIGDLVWGKIKGFSWWPAMVVSWKATSKRQAMPGMRWVQWFGDGK
SEISADKLVAFGLEFGQHFNILATFNKLVSYSKRAMFATTARAKARAGKFTSSSPGGESLED
QLLKPMLEWALGGFFGTFGLEFKOFWKKQPERKSRRTTNDSAASESPPKRLKTNSYGG
KORGEDEESRRMASEVTNNKGNLEDRCLSCGKKNPVSFPPLFEGGLCQSCRDRFLEL
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CYMCLPQRCHQFURRRKDWNRLQDFFTTDPDLEBFBEPRLYPAIPAAKRREITRVLSL
FDGIATGYLVLKELGIKVEKYYNSEVCASIAVGHYKHEGGIKYNDDVRKITKKNIE
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AHYTDVSNMGRGARQKLGRSWSVPYIRHLFAPLKDYFACE"

1113 c 1154 g 956 L
AF151970 4278 bp mRNA linear ROD 08-JUN-2000 Mus musculus DNA cytosine-specific methyltransferase isoform 2 (Dnmt3b) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
P.R.China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon start=1
product="DNA cytosine-specific methyltransferase isoform
                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I. (Dases 1 to 4778)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 4278)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
                                                                                                                                                                                                                                                                                            Cloning of full-length Dnmt3b cDNA and its alternative splicing isoforms in mouse embryonic tissue Unpublished
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/gene="Dnmt3b"
/function="methylates cytosine in DNA"
/note="alternatively spliced"
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Mismatches:
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/dev_stage="8-9 day old embryo"
1. .4278
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                                                                                                AF151970.1 GI:8347119
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360 1491	HisGlyGlyPheLysProThrGlyIleGluGly:	341 1432	음 성
340 1431	lyLysThrPheSerSerSerProGlyGluSerLeuGluAspo 	7 2	유
320 1371	euValSerTyrArgLysAlaMetTyrHisThrLeuGluLysA 		음 성
300	la LeuGly LeuPheSerGlnHisPheAsnLeuz 	281 1252	유상
280 1251	MetProGlyMetArgTrpValGlnTrpPheGlyAspGlyL 	26 119	유 성
260 1191	TrpProAlaMetValValSerTrpLy TGGCCTGCCATGGTGGTGTCCTGGAA	24	B S
240 1131	31uTyrG1nAspAspLysG1uPheG1yI1eG1yAspI 		용 성
220	.uGlyMetAspThrThrGlnValAspAlaGluS 	<u> </u>	유 성
200	ValThrProLysSerValSerThrProSerVa 	181 952	유왕
180 · 951	rgArgAlaSerSerSerAlaSerThrProTrp 	161 892	용성
160 891	HisValGlnGluTyrProValGluPhe 	141 832	음 성
140 831	/ThrSerSerLeuGluArgGlnArgAlaSer 	121 772	유 성
120 [°] 771	rgThrArgSerGlu GACGCGCTCTGAA	712	음_성
100	;luValaspaspGlyasnGly 	81 652	유 성
80 651	SerSerSerArgLeuSerLysArgGluValSerSerLeuLeuAsnTyrThrGlnAspMet 	61 592	유왕
60 591	uProValCysThrPro GCCAGTCTGCACACCA	41 532	유 성
40 531	snPheSerAspGlnSerSerAspThri ACTTCAGTGACCAGTCCTCAGACACG	21 472	유 성

741 PheTrpGlyAsnLeuProGlyMetAsnArgProValMetAlaSerLySAsnAspLySLeu 760	γ
CATGTAACCCAGTGATGATGGATGCCATCAAGGTGTCTGCTGCTCACAGGGCCCGGTA	뫄
721 AlaCysAsnProValMetIleAspAlaIleLysValSerAlaAlaHisArgAlaArgTyr 740	γQ
701 MetPheGluAsnValValAlaMetLysValAsnAspLysLysAspIleSerArgPheLeu 720	당 양 양
TITTACCACTTGCTGAATTATACCCGCCCAAGGAGGGGGACAACCGTCCATTCTTCTGG 2451	p 5
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72 AATATTGAAGAGTGGGGCCCGTTCGACTTGGTGATTGGTGGAAGCCCATGCAATGATCTC 23	}
snIleGluGluTrpGlyProPheAspLeuValIleGlyGlySerProCysAsnAspLe	δδ
621 ThrValLysHisGluGlyGlnIleLysTyrValAsnAspValArgLysIleThrLysLys 640	ρ Q
52 GGTATTAAAGTGGAAAAGTACATTGCCTCCGAAGTCTGTGCAGAGTCCATCGCTGTGGGA 22	B 4
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21 AlaLysLeuGlnGluProTrpSerCysTyrMetCysLeuProGlnArgCysHisGlyVal 5	g 9
52 TGCAGATGCTTCTGTGGAGGTGTCTGGAGGTGGTGGTGGGCGCAGGCACAGCTGAGGAT 19	DP K
TCCTACTGCACCGTGTGCTGTGAGGGCCGTGAACTGCTGCTGCTGTAACACAAGCAAG	
81 SerTyrCysThrValCysCysGluGlyArgGluLeuLeuLeuCysSerAsnThrSerCys 50	\$ 8
461 GINSerCysArgAspArgPheLeuGiuLeuPheTyrMetTyrAspGiuAspGiyTyrGin 480	dd Vy
72 TTGTCCTGTGGAAAGAACCCTGTGTCCTTCCACCCCCTCTTTGAGGGTGGGCTCTGT 17	망
41 LeuSerCysGlyLysLysAsnProValSerPheHisProLeuPheGluGlyGlyLeuCys 46	· Qγ
421 SerArgGluArgMetAlaSerGluValThrAsnAsnLysGlyAsnLeuGluAspArgCys 440	ρ γ
52 CCACCCAAGCGCCTCAAGACAAATAGCTATGGCGGGAAGGACCGAGGGGAGGATGAGGAG 16	문
LeuLysThrA 	δ
1498GAGAACAAAAGTCGAAGACGCACAACCAATGACTCTGCTTCTGAGTCCCCC 1551	DЬ

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Mus musculus DNA cytosine methyltransferase 3b6 (Dnmt3b6) mRNA, Complete cds; alternatively spliced.
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SEI SADKLVALGLFSQHFNLATFNKLVSYRKAMYHTLEKARNKRAGKFPSSSPGESLED
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SRRRRASSSASTPWSSPASVDFWEEVTPKSVSTPSVDLSQDGDQEGMDTTQVDAESRD
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LEVLVGAGTAEDAKLQEPWSCYMCLPQRCHGVLRRRKDWNMRLQDFFTTDPDLEEFEP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4006)
Chen, T., Ueda, Y. and Li, E.
Dintala2 encoded by transcripts from an intronic promoter of Dnmt3a is expressed abundantly in ES cells and germ cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen,T., Ueda,x. and Li.L.
Direct Submission
Submitted (08-FEB-2002) Cardiovascular Research Center,
Massachusetts General Hospital, 149 13th Street, Charlestown, MA
                                                                                                                                                                    2692 ACCACCAAGTCGAACTCCATCAGACAGGCAAAAACCAGCTTTTCCCTGTAGTCATGAAT 2751
                                                                                                                                                                                                                                                                2752 GGCAAGGACGATGTTTTGTGGTGCACTGAGCTCGAAAGGATCTTCGGCTTCCCTGCTCAC 2811
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2572 TTCTGGGGTAACCTACCCGGAATGAACAGGCCCGTGATGGCTTCAAAGAATGATAAGCTC 2631
                                                                                       GlyLysAspAspValLeuTrpCysThrGluLeuGluArgllePheGlyPheProAlaHis 820
                                                                                                                                                                                                                                                                                                                         TyrThrAspValSerAsnMetGlyArgGlyAlaArgGlnLysLeuLeuGlyArgSerTrp 840
                                                                                                                                      ThrThrLysSerAsnSerIleArgGlnGlyLysAsnGlnLeuPheProValValMetAsn 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="de novo methylation"
/note="contains PHD and PWWP domains; alternatively
                                                                                                                                                                                                                                                                                                                                                                                                                   SerValProValIleArgHisLeuPheAlaProLeuLysAspTyrPheAlaCysGlu 859
                                            GluLeuGlnAspCysLeuGluPheSerArgThrAlaLysLeuLysLysValGlnThrIle
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protein id="AAL85481.1"
db_xref="G1:21655121"
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/db_xref="taxon:10090"
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n,T., Ueda,Y. and Li,E.
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'gene="Dnmt3b6"
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/codon_start=1
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EGQIKYVNDVAKXTKKNIEEMGPPDLVIGGSPCNDLSNVNPARKGLYEGTGRLFFEFY
HLLNYTRPKEGDNRPFFWFENVAMKVNDKKDISRFLACNPVMIDAIKVSAAHRARY
FWGNLPGWNRIFGFPAHYTDVSNMGRARGARGKLLGRSWSVPVIRHLFAPLKDYFACE"

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                                                                                                                                                                                                                                                                                                                                                      329 ATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACGAAGGATGCTCCTCACCC
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Mammalia; Eutheria; Rodentia; S:
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Yin,B., Chen,Y.T., Zhu,M., Luo,
Shen,Y.
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Yin,B, Chen,Y.T., Zhu,M.,
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Cloning of full-length Dnmt3b
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Submitted (17-MAY-1999)
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Medical Sciences, Dong D
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Mus musculus DNA cytosine-specific (Dnmt3b) mRNA, complete cds.
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1197 AAGCTGGTTTCTTATAGGAAGGCCATGTACCACACTCTGGAGAAAGCCAGGGTTCGAGCT
                                                                   837 GACTTCATGGAAGAAGTGACACCTAAGAGCGTCAGTACCCCATCAGTTGACTTGAGCCAG
                                                                                                                AspGlyAspGlnGluGlvGlyMetAspThrThrGlnValAspAlaGluSerArgAspGlyAsp
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AspPheMetGluGluValThrProLysSerValSerThrProSerValAspLeuSerGln
                                                                                                                                                  SerThrGluTyrGlnAspAspLysGluPheGlyIleGlyAspLeuValTrpGlyLysIle
                                                                                                                                                                                                                 957 AGCACAGAGTATCAGGATGATAAAGAGTTTGGAATAGGTGACCTCGTGTGGGGAAAGATC
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Mus musculus DN;
(Dnmt3b) mRNA, a
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                                                                                                                                                                 1 MetLysGlyAspSerArgHisLeuAsnGluGluGluGlyAlaSerGlyTyrGluGluCys
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ProValLeuGluAlaIleCysThrGluProValCysThrProGluThrArgGlyArgArg
                                                             ATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACGAAGGATGCTCCCTCACCC
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 4149)

Yin,B., Chen,Y.T., Zhu,M., Luo,Y.J., Zhu,N., Xu,S.C., Wu,G.Y. and Shen,Y.

Cloning of full-length Dnmtlb cDNA and its alternative splicing isoforms in mouse embryonic tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-MAY-1999) Department of Biochemistry and Molecular Biology, Institution of Basic Medical Sciences, Chinese Academy (Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 4149)
Yin, B., Chen, Y.T., 2
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SEISADKLVALGLFSQHFNLATFNKLVSYRKAMYHTLEKARVRAGKTESSSPGESLED
QLKPMLEWAHGGFKPTGIEGLKPNKKQPVVNKSKVRSDSRNLEPRRENKSRRRTTN
DSAASESSPPEKRLKTNSYGGKDRGEDESSREWASEVTNNKGNLEDRCLSCGKKNPVS
FHPLFEGGLCQSCRDRFLELFYMYDEDGYQSYCTVCCEGRELLLCSNTSCCRCFCVEC
LEVLVGAGTNAEDAKLQEBWSCYMCLEQRCHGVLRRRKDWNRRLQDFFTTDDPLEEFEE
PKLYPAIFAAKKRPIRVLSLFDGIATGYLVLKELGIKVEKYIASEVCABSIAVGTVKH
EGQIKYNNDVRKITKKNIEBWGPFDLVIGGSPCNDLSNVNPARKGLYEGTGRLFFEFY
HLLNYTRPKEGDNRPFFWMFENVVAMKVNDKKDISRFLACHSPWIDJAIKVSAAHRARY
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LTRETKDTRTRSESPAVRTRHSNGTSSLERQRASPRITRGRQGRHHVQEYPVEFPATR
SRRRRASSSASTPWSSPASVDFMEEVTPKSVSTPSVDLSQDGDQEGMDTTQVDAESIY
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/db_xref="GI:8347126"
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|"
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ò		PheHisProLeuPheGluGlyGlyLeuCys 4	091
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ò 8	7	Phenyimecnyiaspendaspenyiyidin 4 	851
ò		GlubeuleuleuCysSerAsnThrSerCys 5	009
q	-	GAACTGCTGTGCAGTAACACAAGCTGC 1	1611
δλ		ValLeuValGlyAlaGlyThrAlaGluAsp 5	250
q	-	grecigeredececacacreaders	1971
ò		MetCysLeuProGlnArgCysHisGlyVal 5	040
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ò		LeuglnAspPhePheThrThrAspProAsp 5	099
QQ	(A)	crecaagacricricacracrearccigae	2091
ò		ProAlaileProAlaAlaLysArgArgPro	280
QQ	N	ccascaatrectscasccaaaassassecc	2151
ò		AlaThrGlyTyrLeuValLeuLyBGluLeu (009
qq	i,	scaacederactrestecreaadeaetre	2211
ò		GluvalCysAlaGluSerIleAlaValGly (620
g	"	saagreterscadadrecarescretesa z	2271
ò		ValAsnAspValArgiysileThrLysiys (640
Q	.,	Grcaargacarcegaaaarcaccaagaaa 2	2331
ŏ		ValileGlyGlySerProCysAsnAspLeu (099
qq	**	ercharradradaccaracantarere	2391
ò		TyrgluglyThrGlyArgLeuPhePheGlu	680
g	**	ratcadedcacadadecterretread	2451
ò			700
qq	•	zakdokodokokakokatokatoka :	2511
ò		AsnasplyslysasplleSerargPheleu	720
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ò		LysvalSerAlaAlaHiBArgAlaArgTyr	740
d		sakdardrefertekcadaddeceedrae	2631
ò		yProValMetAlaSerLysAsnAspLysLeu	760
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ò		ThrAlaLysLeuLysLysValGlnThrIle	780
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                                                                                                                                                                                                                                                                                                                                              Charlestown, MA 02129, USA
Sequence update by submitter
On Nov 18, 1999 this sequence
Location/Qualifiers
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Okano, M., Chijiwa, T., Sasaki, H.
                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (04-NOV-1999)
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Direct Submission
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Okano, M., Xie, S. and Li, E.
Cloning and characterization of a family
(Cytosine-5) methyltransferases
Nat. Genet. 19 (3), 219-220 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to
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/translation="MKGDSRHLNEEEGASGYEECIIVNGNFSDQSSDTKDAPSPPVLE
AICTEPVCTPETRGRRSSSRLSKREVSSLLNYTQDMTGDGDRDDEVDDGNGSDILMPK
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SRRRRASSSASTPWSSPASVDFMEEVTPKSVSTPSVDLSQDGDQEGMDTTQVDAESRD
                                                                                                                                                                            /note="similar to EST sequences deposited in GenBank Accession Numbers AA116694, AA119979, AA177277, AA21 AA407106, and AA575617"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Butheria;
                                                      /codon_start=1
/product="DNA cytosine-5
/protein_id="AAC40180.2"
/db_xref="GI:6449474"
                                                                                                                                                                                                                                              /gene="Dnmt3b"
                                                                                                                       /function="de novo DNA methylation"
/note="alternatively spliced product;
                                                                                                                                                                                                                                                                           /map="84.0 cM"
                                                                                                                                       function="de novo
                                                                                                                                                    gene="Dnmt3b"
                                                                                                                                                                                                                       gene="Dnmt3b"
                                                                                                                                                                                                                                                                                          chromosome="2"
                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
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GDSTEYQDDKEFGIGDLVWGKI KGFSWWPAMVVSWKATSKRQAMPGMRWVQWFGDGKF
SEISADKLVALGLFSQHFNLATFNKLVSYRKAMYHTLEKARVRAGKTFSSSPGESLED
QLKPMLEWAHGGFKPTGI EGLKPNKKQPENKSRRRTTNDSAASESPPPKRLKTNSYGG
KDRGEDEESREMASEYTNNKCHLEDRCLGSGKKNPYSFHPLF EGGLCQSCRDRFLEL
FYMYDEDGYQSYCTVCCEGRELLLCSNTSCCRCFCVECLEVLVGAGTAEDAKLQEPWS
CYMCLFQRCHGVLERRKDWNNRLQDFFTTDPDLEEFEPPKLYPALIPAKRRFIXVLSL
FDGIATGYLVLKELGIXVEKYIASEVCAESIAVGTVKHEGQIKYVNDVRKITKKNIEE
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ENVVAMKVNDKKDISRFLACNPVMIDAIKVSAAHRARYFWGNLPGMNRIFGFPAHYTD
VSNMGRGARAKKLLGRSWSVPVIRHLFAPLKDYFACE"

a 1006 c 1056 g 901 t

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Percent Similarity:
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Query Match:
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                                                                                     SerThrGluTyrGlnAspAspLysGluPheGlyIleGlyAspLeuValTrpGlyLysIle
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                                                         AGCACAGAGTATCAGGATGATAAAGAGTTTGGAATAGGTGACCTCGTGTGGGGAAAGATC
                                                                                                                                GATGGAGATCAGGAGGGTATGGATACCACACAGGTGGATGCAGAGAGCAGAGATGGAGAC
                                                                                                                                                        AspGlyAspGlnGluGlyMetAspThrThrGlnValAspAlaGluSerArgAspGlyAsp
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g	989 AAGG	AAGGCCTTCTCCTGGTGGCCTGCCATGGTGGTGTTCCTGGAAAGCCACCTCCAAGCGALAG
<u></u>	261 Alam 1049 GCCA	WetProdlyMetArgTrpValdInTrpPhedlyAspdilyLysPheserdilieser 280
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ጵ ጵ	301 LysL 1169 AAGC	ceuvalserTyrArgLysAlaMetTyrHisThrLeuGluLysAlaArgValArgAla 320
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: À	421 SerA	argGluArgMetAlaSerGluValThrAsnAsnLysGlyAsnLeuGluAspArgCys 440
ą	1469 AGCC	
<u>ک</u> ۾	441 Leus 1529 TTGT	SerCysGlyLysLysAsnProValSerPheHisProLeuPheGluGlyGlyLeuCys 460
ጵ ጵ	461 GlnS 1589 CAGA	SerCysArgAspArgPheLeuGluLeuPheTyrMetTyrAspGluAspGlyTyrGln 480
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3 6	501 CYBA	ArgCysPheCysValGluCysLeuGluValLeuValGlyAlaGlyThrAlaGluAsp
2 2	521 Alan	UysLeuGlnGluProTrpSerCysTyrMetCysLeuProGlnArgCysHisGlyVal 540
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2 2	581 IleA 1949 ATTA	argvalLeuSerLeuPheAspGly1leAlaThrGlyTyrLeuValLeuLysGluLeu 600
ጵ ል	601 GlyI 2009 GGTA	GlyileLysValGluLysTyrIleAlaSerGluValCysAlaGluSerIleAlaValGly 620

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3974 bp mRNA linear ROD 08-JUN-2000 Mus musculus DNA cytosine-specific methyltransferase 160form 8 AF151976
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Direct Submission
Sybnitced (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Bukaryota, Metazoa, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 3974)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
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Unpublished
2 (bases 1 to 3974)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
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621 ThrvallysHisGluGlyGlnIleLysTyrValAsnAspValArgLysIleThrLysLys 640
1069 ACTGTTAAGCATGAAGGCCAGATCAAATATGTCAATGACGTCCGGAAAATCACCAAGAAA 2128
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SEISADKLVALGLFSQHFNLATFNKLVSYRKAMYHTLEKARVRAGKTFSSSPGESLED
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CYMCLPQRCHGVLRRRKDWMRLQDFFTTDPDLEEFPPKLYPAIPAKRREIRVLSL
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501 CysArgCysPheCysValGluCysLeuGluValLeuValGlyAlaGlyThrAlaGluAsp 520
                                                 521 AlaLysLeuGlnGluProTrpSerCysTyrMetCysLeuProGlnArgCysHisGlyVal 540
                                                                                                                                                                                                                                                                                                        ThrvalLysHisGluGlyGlnIleLysTyrValAsnAspValArgLysIleThrLysLys 640
                                                                                                                                                                                                                                                                                                                                                         641 AsnIleGluGluTrpGlyProPheAspLeuValIleGlyGlySerProCysAsnAspLeu 660
                                                                                                                                                                                                                                                                                                                                                                                                         SerAsnValAsnProAlaArgLysGlyLeuTyrGluGlyThrGlyArgLeuPhePheGlu 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   761 GluLeuGlnAspCysLeuGluPheSerArgThrAlaLysLeuLysLysValGlnThrIle 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                821 TyrThrAspValSerAsnMetGlyArgGlyAlaArgGlnLysLeuLeuGlyArgSerTrp 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetPheGluAsnValValAlaMetLysValAsnAspLysLysAspIleSerArgPheLeu 720
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                                                                                                               1917 CTGGAAGAATTTGAGCCACCCAAGTTGTACCCAGCAATTCCTGCAGCAAAAGGAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                          2217 TCTAACGTCAATCCTGCCCGCAAAGGTTTATATGAGGGCACAGGAAGGCTCTTCTTCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuGluGluPheGluProProLysLeuTyrProAlaIleProAlaAlaLysArgArgPro
                                                                                                                                                                                                      581 IleArgValLeuSerLeuPheAspGlyIleAlaThrGlyTyrLeuValLeuLysGluLeu
                                                                                                                                                                                                                             1977 Arragagrecrerererricardaaarrecaacedegracriderecraaddaerre
                                                                                                                                                                                                                                                      GlyIleLysValGluLysTyrIleAlaSerGluValCysAlaGluSerIleAlaValGly
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4089 bp mRNA linear ROD 08-JUN-2000 Mus musculus DNA cytosine-specific methyltransferase isoform 3 (Dnmt3b) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein id="AAF74517.1"
/db_xref="GI:8347123"
/translation="MKGDSRHLNEEEGASGYEECIIVNGNFSDQSSDTKDAPSPPVLE
                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="DNA cytosine-specific methyltransferase isoform
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (abses 1 to 4089)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
                                                                                                                                                                                                                                                           2 (bases 1 to 4089)
Yin,B., Chen,Y.T., Zhu,M., Luo,Y.J., Zhu,N., Xu,S.C., Wu,G.Y. and Shen,Y.
                                                                                                                                                                                             Cloning of full-length Dnmt3b cDNA and its alternative spliting isoforms in mouse embryonic tissue Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="methylates cytosine in DNA"
note="alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="KM"
/db_xref="taxon:10090"
/dev_stage="8-9 day old embryo"
                                                                                                                                                                                                                                                                                                                                                                                                 1. .4089
/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="Dnmt3b"
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                                                                              AF151971.1 GI:8347122
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4088.50
90.10%
90.10%
89.07%
                                                                                                              Mus musculus.
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Best Local Similarity:
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741 Phe	γQ	1932 CHACA	, ,
2512 GC/	Db	y 361 GlnProValValAsnLysSerLysValArgArgSerAspSerArgAsnLeuGluProArg 38	, S
721 Ala	Q	1432 GAGTGGGCCCACGGTGGCTTCAAGCCTACTGGGATCGAGGGCCTCAAAGCCAACA	<u> </u>
	gg	341 GluTrpAlaHisGlyGlyPheLysProThrGlyIleGluGlyLeuLysProAsnLysLys 36	ş
	Ş	72 GGCAAGACCTTCTCCAGCAGTCCTGGAGAGTCACTGGAGGACCAGCTGAAGCC	뫄
2392 TT	Db .5	321 GlyLysThrPheSerSerSerProGlyGluSerLeuGluAspGlnLeuLysProMetLeu 34	S
_ ,	0 8	CTGGTTTCTTATAGGAAGGCCATGTACCACACTCTGGAGAAAGCCAGGGT	맑
	J (Oy 301 LysLeuValSerTyrArgLysAlaMetTyrHisThrLeuGluLysAlaArgValArgAla 320	Ó
	? ;	CAAACTGGTGGCTCTGGGGCTGTTCAGCCAGCACTTTA	gg
041 ABI	, S	SerGlnHisPheAsnLeuAlaThrPl	S
	ם מ	Db 1192 GCCATGCCCGGAATGCGCTGGTACAGTGGTTTGGTGATGGCAAGTTTTCTGAGATCTCT 1251	밁
621 Thi	. 29	Qy 261 AlaMetProGlyMetArgTrpValGlnTrpPheGlyAspGlyLysPheSerGluIleSer 280	Q
52	Db		Db
601 Gl	δλ	241 LvsGlvPheSerTrpTrpProAlaMetValValSerTrpLvsAlaThrSerLvsArqGln 2	o O
2092 ÅT	дb		멍
581 I1e	Qy	221 SerThrGluTyrGlnAspAspLysGluPheGlyIleGlyAspLeuValTrpGlyLysIle 2	S S
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561 Leu	Qy	201 BenGlyBenGlyGlyGlyMor*BendhydhyglyValanalaglyCoxyXyaXayClyCax	2 1
N	DЪ	952 GACTTCATGGAAGAAGTGACACCTTAAGACCCCTTAAGTACCCCATTGACTTGAACCTTAAGACACTTGAACTTGAACCTTGAACACTTGAACACTTGAACACTTGAACAACTTGAACAACAACAACAACAACAACAACAACAACAACAACAAC	B 4
541 Let	VQ	181 AsnoheMetGliiGliiValThrbroTvsSarValSerThrbroSerValAsnieiiSerGli 20	2 1
1912 GCC	ф	\(\frac{\partial}{\partial}\) \qq \q	로 5
521 Ala	νο	832 CGAGGTCGGCAGGGCCGCCACCATGTGCAGGAGTACCCTGTGGAGTTTCCGGCTACCAGG 89) <u> </u>
1852 TGC	Db	141 ArgGlyArgGlnGlyArgHisHisValGlnGluTyrProValGluPheProAlaThrArg 16	. <i>.</i> 6
501 ÇY8	S S	772 ACCCGACATAGCAATGGGACCTCCAGCTTGGAGAGGGCAAAGAG	g
1792 TCC	문	121 ThrargHisSerAsnGlyThrSerSerLeuGluArgGlnArgAlaSerProArgIleThr 14	. 6
481 Set	? E		말
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1672 770	D, K	Oy 81 ThrGlyAspGlyAspArgAspAspGluValAspAspGlyAsnGlySerAspIleLeuMet 100	γQ
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j	Q	SerSer	8
N	DЬ	532 CCAGTCTTGGAGGCAATCTGCACAGAGCCAGTCTGCACACAGAGACCAGAGGCCGCAGG 5	밁
401 Pro	Оу	41 ProValLeuGluAlaIleCvsThrGluProValCvsThrProGluThrArgGlvArgArg 60	, ô
1498	qq	OY 21 IleIleValAsnGlyAsnPheSerAspGlnSerSerAspThrLysAspAlaProSerPro 40	B 8
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1 PheTrpGlyAsnLeuProGlyMetAsnArgProValMetAlaSerLysAsnAspLysLeu 	7	
21 AlaCysasnProValMetIleAspAlaIleLysValSerAlaAlaHisArgAlaArgTyr 7	Qy 72 Db 251	
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81 PheTyrHisLeuLeuAsnTyrThrArgProLysGluGlyAspAsnArgProPhePheTrp 7	Qy 68 Db 239	
61 SerAsnValAsnProAlaArgLysGlyLeuTyrGluGlyThrGlyArgLeuPhePheGlu 6 	Qy 66 Db 233	
41 AsnileGluGluTrpGlyProPheAspLeuVallleGlyGlySerProCysAsnAspLeu 6	Qy 64 Db 227	
21 ThrVallysHisGluGlyGlnIleLysTyrValAsnAspValArgLysIleThrLysLys 6	Qy 62 Db 221	
01 GlyIleLysValGluLysTyrIleAlaSerGluValCysAlaGluSerIleAlaValGly 6 	Оу 60 Дь 215	
81 IleArgValLeuSerLeuPheAspGlyIleAlaThrGlyTyrLeuValLeuLysGluLeu 60 	Qy 58 рь 209	
51 LeuGluGluPheGluProProLysLeuTyrProAlaIleProAlaAlaLysArgArgPro 58 	Qy 56 рь 203	
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11 LeuSerCysGlyLysLysAsnProValSerPheHisProLeuPheGluGlyGlyLeuCys 46 	Qy 44 Db 167	
21 SerArgGluArgMetAlaSerGluValThrAsnAsnLysGlyAsnLeuGluAspArgCys 44 	Oy 42 Db 161	
31 ProProLysArgLeuLysThrAsnSerTyrGlyGlyLysAspArgGlyGluAspGluGlu	Oy 40 Db 155	
	Db 149	

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4145 bp mRNA linear PRI 05-SEP-1999
Homo sapiens DNA cytosine-5 methyltransferase 3 beta 1 (DNMT3B)
AF156488
AF156488.1 GI:5823167
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PPSSYLTIDLTDDTEDTHGTPQSSSTPYARLAQDSQGGGRESPQVEADSGDGDSSEYQ
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CPAPKRLKTNCYNNGKDRGDEDGSREGMASDVANNKSSLEDGCLSCGRKNPVSFPLF
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I PAARRRPIRVLSLFDGIATGYLVLKELGIKVGKYVASEVCEESIAVGTVKHEGNIKY
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LVALGLFSQHFNLATFNKLVSYRKAMYHALEKARVRAGKTFPSSPGDSLEDQLKPMLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (03-JUN-1999) CVRC, Mass. Gen. Hospital, 149 13th Street,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Xie, S., Wang, Z., Okano, M., Nogami, M., Li, Y., He, W.W., Okumura, K. and Li, E.
                                                                                                                                                                                                                                             2599 -----AGGATCTTCGGCTTCCCTGAC 2622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression and chromosome locations of the human DNMT3
                                        761 GluLeuGlnAspCysLeuGluPheSerArgThrAlaLysLeuLysLysValGlnThrIle 780
                                                                                                                              781 ThrThrLysSerAsnSerIleArgGlnGlyLysAsnGlnLeuPheProValValMetAsn 800
                                                                                                                                                                                                                      801 GlyLysAspAspValLeuTrpCysThrGluLeuGluArgllePheGlyPheProAlaHis 820
                                                                                                                                                                                                                                                                                                       821 TyrThrAspValSerAsnMetGlyArgGlyAlaArgGlnLysLeuLeuGlyArgSerTrp 840
                                                                                                                                                                                                                                                                                                                                                                                                                      2683 AGIGTACCGGTCATCAGACACCTGTTTGCCCCCTTGAAGGACTACTTTGCCTGTGAA 2739
                                                                                                                                                                                                                                                                                                                                                                                            841 SerValProValIleArgHisLeuPheAlaProLeuLysAspTyrPheAlaCysGlu 859
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/organism="Homo sapiens"
/db_xref="teaxon:9606"
/db_tromosome="20"
/map="between D20S182 and D20S106; 39.9-50.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="de novo DNA methyltransferase"
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Location/Qualifiers
2572 TTCTGGGGTAACCTACCCGGAATGAAC--
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gene family
Gene 236 (1), 87-95 (1999)
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/gene="DNMT3B"
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Xie,S. and Li,E.
Direct Submission
Submitted (03-JUN-1999
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VNDVRNITKKNIEEWGPFDLVJGGSPCNDLSNVNPARKGLYEGTGRLFFEFYHLLNYS
RPKEGDRPFFWWFENVVAMKVGDKRDISRFLECNPVNIDAIKVSAAHRARYFWGNLP
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VLMCTELERIFGFPVHYTDVSNMGRGARQKKLLGRSWSVPVIRHLFAPLKDYFACE"
1083 c 1096 g 925 L
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                                                                        2 (bases 1 to 4335)
Ni,J., Pradhan,S. and Robert
Direct Submission
Submitted (22-DEC-2000) New
                                                                                                                                       Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 4335)
Ni,J., Pradhan,S. and Roberts,
Cloning, expression and charac
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Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature (1999) In press 2 (bases 1 to 4267) Xu,G.L. and Bestor,T.H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 4267)
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RATASAGTEWAPS PASSYLIT I DLTDDTEDTHGTHGTPQSSSTPYARLAQDSQQGGWES PQVE
ADSGDGDSSEY QDGKE PGIGDL VWGKI KGFSWWP PAMVYSWKATSKRQAMSGMEW VQWF
GDGKFSEVSAD KLVALGLFSQHFINLATFINKLVS YRKAMYHALLEKARVRAGKTEPSSPG
GDGKFSEVSAD KLVALGLFSQHFINLATFINKLVS YRKAMYHALLEKARVRAGKTEPSSPG
DSLEDQLKPMLEWAHGGFKPTGI EGLKPNINTQ PENKTRRTADDSATSDYCPA PKRLK
TNCYNINGKURGDDDQSREQMASDVANNKSSLEDGCLSGGRKNEVSFHPLFEGGLCQTC
RDRFLELFYMYDDDGYQSYCTVCCEGRELLLCSNTSCCRCFCYCCLEVLVGTGTAAEA
KLQEPWSCYMCLPQRCHGVLRRRKDMNVRLQAFFTSDTGLEYEAPKLYPAI PAARRRP
IRVLSLFDGI ATGYLVLKELGI KVGKYVASEVCEESI AVGTVKHEGNI KYVNDVRNI T
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RIFGFFVHYTDVSNMGRGARQKLLGRSWSVPVI RHLFAPLKDYFACE"
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DSPPILEAIRTPEIRGRRSSSRLSKREVSSLLSYTQDLTGDGDGEDGDGSDTPVMPKL
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/protein_id="AAF04015.1"
/db_xref="GI:6118092"
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14-AUG-1996

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entry)

AAT21884 ID AAT21884 standard;

AAT21884;

CDNA to mRNA; 301 ВP

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. Human gene signature HUMGS03426

Homo sapiens.

01-JUN-1995

11-NOV-1994; 94WO-JP01916.

12-NOV-1993; 93JP-0355504.

(MATS/) MATSUBARA K. (OKUB/) OKUBO K.

Okubo K;

WPI, 1995-206931/27.

Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human e 9

Claim 1; Page 991-992; 2245pp; Japanese

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) from various human tissues; synthesis of cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. different mRNAs in the particular tissue The appearance frequency of a given GS in determined (esp. using primers and probes probes derived in a cDNA library from the င္သ be.

> SSSS Sequence 301 BP; 96 A; 65 C; 63 G; sequences) as a means of diagnosing abnormal cell function or for recognising different cell types. 66 T; 11 other;

Query Match Best Local Similarity Matches 241; Conserv Conservative 4.2%; 0 Score 177.4; DB Pred. No. 3.9e-33 Mismatches DB 16; Length 301; Indels 6 Gaps

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3453 GATCAGATAGGAGCACAAACAGGAAGAGAATAGAGA---CCCTCGGAGGCAGAGTCTCCT 3509 _

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and Li,E.
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1 (bases 1 to 4145)

Xie, S., Wang, Z., Okano, M., Nogami, M., Li, Y., He, W.W., Okumura, K.
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Direct Submission
Submitted (03-JUN-1999) CVRC, Mass.
Charlestown, MA 02129, USA
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VANGR PVLASKNDKLEGGF PV HYTDVSNNGRGARQKLLGRSWSVPVIRHLFAPLKDYFACE"
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                             ArgArgThrAlaAspAspSerAlaThrSerAspTyrCysProAlaProLysArgLeuLys
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1915 1855 441 LysAsnProValSerPheHisProLeuPheGluGlyGlyLeuCysGlnThrCysArgAsp 460 2215 2155 2095 1675 109 581 PheAspGlyIleAlaThrGlyTyrLeuValLeuLysGluLeuGlyIleLysValGlyLys 600 701 AlaMetLysValGlyAepLysArgAspIleSerArgPheLeuGluCysAsnProValMet 681 TyrSerArgProLysGluGlyAspAspArgProPhePheTrpMetPheGluAsnVallVal 700 521 ProTrpSerCysTyrMetCysLeuProGlnArgCysHisGlyValLeuArgArgArgLys 540 741 GlyMetAsnArgProVallleAlaSerLysAsnAspLysLeuGluLeuGlnAspCysLeu 760 TyrvalAlaSerGluValCysGluGluSerIleAlaValGlyThrValLysHisGluGly 620 ValGluCyBLeuGluValLeuValGlyThrGlyThrAlaAlaGluAlaLySLeuGlnGlu 520 ProPheAspLeuVallleGlyGlySerProCysAsnAspLeuSerAsnValAsnProAla 660 720 2034 1854 1794 1734 1494 1434 1374 2334 740 2274 2154 680 2094 640 1914 1674

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	S CACCTCTTCGCCCCTCTGAAGGACTACTTTGCATGTGAA 2673	2635	용
	HisLeuPheAlaProLeuLysAspTyrPheAlaCysGlu 853	841	ş
ر در در	ATGGGCCGTGGTGCCCGCCAGAAGCTGCTGGGAAGGTCCTGGAGCGTGCCTGTCATCC	2575	밁
- 8 - 6 - 17	821 MetGlyArgGlyAlaArgGlnLysLeuLeuGlyArgSerTrpSerValProValIleArg 840	82:	ફ
AC 2574	TGGTGCACTGAGCTCGAAAGGATCTTTGGCTTTTCCTGTGCACTACACAGACGTGTCCA	251	용
\sn 820	801 TrpCysThrGluLeuGluArgIlePheGlyPheProValHisTyrThrAspValSerAsn	80:	δ
rrg 2514	ATCAAACAGGGAAAAACCAACTTTTCCCTGTTGTCATGAATGGCAAAGAAGATGTTT	2455	日
Leu 800	IleLysGlnGlyLysAsnGlnLeuPheProValValMetAsnGlyLysGluAspValLeu	781	ફ
	GAATACAATAGGATAGCCAAGTTAAAGAAAGTACAGACAATAACCACCAAGTCGAACT	2395	8
- řer - 7	GluTyrAsnArgIleAlaLysLeuLysLysValGlnThrIleThrThrLysSerAsnSer 780	761	8

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Minimum
Maximum
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-Q=/cgn2_1/USPTO_spool/US09720086/runat_18112002_092832_22195/app_query.fasta_1.4252
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-D0CALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-USER=US09720086_@CGN_1_1_11308_@runat_18112002_092832_22195 -NCPU=6 -ICPU=3
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPDET10-XGAPDEXT=0.5 -FGAPDOP=6 -FGAPEXT=7
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1: gb_ba:*

2: gb_htg:*

3: gb_in:*
US-09-720-086-8
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(c) 1993 - 2002 Compugen Ltd
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5107.633 Million cell updates/sec
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em htg_hum: *
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em htg_mus: *
em htg_pln: *
em htg_mam: *
em htg_wrt: *
em htg_vrt: *
em htgo_mus: *
em htgo_mus: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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ALIGNMENTS

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VLWCTELERIFGFPVHYTDVSNMGRGARQNCLFCRSSWSVPVIRHLFAPPLKNDYFACE"
1083 C 1096 G 925 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xie,S. and Li,E.
Direct Submission
Submitted (03-JUN-1999) CVRC, Mass. Gen. Hospital, 149 13th Street,
Charlestown, MA 02129, USA
Location/Qualifiers
          4F156488

Hömo sapiens DNA cytosine-5 methyltransferase 3 beta 1 (DNMT3B)
mRNA, complete cds.
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 4145)
                                                                                                                                                                                                                                                                                    Wang, Z., Okano, M., Nogami, M., Li, Y., He, W.W., Okumura, K.
                                                                                                                                                                                                                                                                                                                                  expression and chromosome locations of the human DNMT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 IleLeuValAsnGlyAlaCysSerAspGlnSerSerAspSerProProIleLeuGluAla 40
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/mb_bromose="20"
/map="between D20S182 and D20S106; 39.9-50.2
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gene family
Gene 236 (1), 87-95 (1999)
99365304
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115. .2676
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AF156488.1 GI:5823167
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Best Local Similarity:
Query Match:
DB:
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VERSION
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SOURCE
ORGANISM
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AF156488'
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TITLE
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175 ATCCTCGTCAACGGGGCCTGCAGCGACCAGTCCTCCGACTCGCCCCCAATCCTGGAGGCT
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PPSSYLTIDLTDDTEDTHGTPQSSSTPYARLAQDSQQGMESPQVEADSGDGDSSEYQ

DGKEFGIGDLVWGKIKGFSWWPAMTVSWKATSKRQAMSGMRWVQWFGDGKEFSDVSADK

LVALGLFSQHFNILATENKLVSYRKAWYHALEKARVRAGKTEPSSPGDSLEDQLKPMLE

WAHGGFRPGIEGLKPNNTQPVNINSKVRRAGSRKLESRKYENKTRRTTADDSATSDY

CPAPKRLKUNCYNINGKDRGDEDQSREQMASDVANINKSSLEDGCLSCGRKNPVSFHPLF

EGGLCQTCRDRFLELFYMYDDDGYGSYCTVCCBERELLLCSNITSCCRCFCVECLEVLV

GTGTAAEAKLQEPSKSCYMCLEQRCHGVLRRRKDMNVRLQAFFTSDTGLEXEAPKLYPA

IPAARRRPIRVLSLFDGIATGYLVLKELGIKVGKYVASEVCEESIAVGTVKHEGNIKY

VNDVRNITIKKNI EEMGPFDLVIGGSPCNDLSNUNPARKGLXEGTGRLFFBFYHLLNYS

RPKEGDDRPFFMMFENVYAMKVGBLISRFLECNPVMIDAIKVSAAHRARYFMGNLP

GMNRPVLASKNDKLELQDCLEYNRIAKLKVQTITTKSNSIKGKOKQLFPFVMGKED

VLMCTELERIFGFPVHYTDVSNMGRGARQKLLGRSWSVPVIRHLFAPLKDYFACE"

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AF176228
                                                                                                                                                                                      Direct Submission
Submitted (06-AUG-1999) Genetics and Development,
University, 701 West 168 St., New York, NY 10032,
Location/Qualifiers
                                                                                                                                                                                                                                                                                   Xu,G.-L., Bestor,T.H., Bourc'his,D., Hsieh,C.-L., Tommerup, Bugge,M., Hulten,M., Qu,X., Russo,J.J. and Viegas-Pequignot. Chromosome instability and immunodeficiency syndrome caused mutations in a DNA methyltransferase gene
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4267)
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                                     immundeficiency disease alternative 5' exon 1B"
 /codon_start=1
/product="DNA cytosine-5
/product="da="hap04015.1"
                                                            'note="mutated in human chromosome
                                                                           gene="DNMT3B"
                                                                                                     gene="DNMT3B"
                                                                                                                             map="20q11-q13"
'protein_id="AAF04015
                                                                                                                                           chromosome="20"
                                                                                                                                                       organism="Homo sapiens"
db_xref="taxon:9606"
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ICF syndrome;
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(DNMT3B) mRNA,
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RATASAGTPMPSPPSSYLTIDLTDDTEDTHGTPQSSSTPYARLAQDSQQGMESPQVE
RADSGDGDSSEYQDGKEEGIGDLVWGKIKGFSWWPAMVVSWKATSKRQAWSGMRWVQWF
GDGKFSEVGARKLVALGLFSQHFNLLFSRRKVTSYRKAMYHALEKARVRAGKTFPSSPG
DSLEDQLKEMLEMAHGGFKPTGIEGLKPNNTQPENKTRRFTADDSATSDYCPAPKRLK
TNCYNNGKDRGDEDQSREQMASDVANNKSSLEDGCLSCGRKNPVSFHPLFEGGLCQTC
RDRFLELFYMYDDDGYQSYCTVCCEGRELLLCSNTSCCRCCFCVECLEVLVGTGTAAEA
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SKNDKLELQDCLEYNRIAKKKVQTTTTKSNSIK QGKNQLFPVVMNGKEDVLMCTELE
RIFGFPWHYTDVSNMGRGARQKLLGRSWSVPVIRHLFAPLKDYFACE"

1069 a 1098 c 1147 g 953 t
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Percent Similarity:
Best Local Similarity:
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	GAlaGlyLysThrPheProSerSer 320 [MGATGGCTGTTTGTCTGTGGCAGG	
LYSG1UPHEG1Y11eG1YASPLeuValTrpG1yLyS11eLySG1yPheS 	AlametTyrHisAlaLeuGluLysAlaArgva;	LysvalargargalaGlySerargLysLeuGlu	CCTTCAGATGTTGCCAACAAGAGGAGCCTGGAAGATGGCTGTTTGTCTTGTGGCAGG 156	ProfipserCysTyrMetCysLeuProGlnArs [
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3897 bp mRNA linear PRI 05-SEP-1999
Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B)
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
I (bases 1 to 3897)
Xie,S., Wang,Z., Okano,M., Nogami,M., Li,Y., He,W.W., Okumura,K.
and Li,E.
Cloning, expression and chromosome locations of the human DNWT3
Gene family
Gene 236 (1), 87-95 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1981 TTTGATGGCATCGCGACAGGCTACCTAAAGAGTTGGGCATAAAGGTAAGAAAG 2040
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                                                     601 TyrValAlaSerGluValCysGluGluSerIleAlaValGlyThrValLy8HisGluGly 620
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                                             ProAlaValArgThrArgAsnAsnAsnSerValSerSerArgGluArgHisArgProSer
                                                                                                                                                           TCCAGTCTGCTAAGCTACACACAGGACTTGACAGGCGATGGCGACGGGGAAGATGGGGAT
                                                                                                                                                                                 SerSerLeuLeuSerTyrThrGlnAspLeuThrGlyAspGlyAspGlyGluAspGlyAsp
                                                                                                                                                                                                                                                 | IleArgThrProGluIleArgGlyArgArgSerSerSerArgLeuSerLysArgGluVal
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                     CCAGCTGTCCGAACTCGAAATAACAACAGTGTCTCCAGCCGGGAGAGGGCACAGGCCTTCC
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Xie, S. and Li, E.
Direct Submission
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CysCysGluGlyArgGluLeuLeuLeuCysSerAsnThrSerCysCysArgCysPheCys
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                                                                                                                           LysAsnProValSerPheHisProLeuPheGluGlyGlyLeuCysGlnThrCysArgAsp
                                                                                                                                                                                              AlaSerAspValAlaAsnAsnLysSerSerLeuGluAspGlyCysLeuSerCysGlyArg
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                                   CGCTTCCTTGAGCTGTTTTACATGTATGATGACGATGGCTATCAGTCTTACTGCACTGTG
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460 1434 1314

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1014 320 1074 300

2386 CACCTCTTGGCCCCTCTGAAGGACTACTTTGCATGTGAA 2424

QQ	1495	TGCTGCGAGGCCCGAGAGCTGCTTTGCAGCAACACGAGCTGCTGCCGGTGTTTCTGT 1554
දු පු	501	ValGlucysLeuGluValLeuValGlyThrGlyThrAlaAlaGluAlaLysLeuGlnGlu 520
දු දු	521	ProTrpSerCysTyrMetCysLeuProGlnArgCysHisGlyValLeuArgArgArgLys 540
රු සි	541	ABDTrpAenValArgLeuGlnAlaPhePheThrSerAspThrGlyLeuGluTyrGluAla 560
දු ද	561	ProLysLeuTyrProAla11eProAlaAlaArgArgArgIto11eargValLeuSerLeu 580
8 % B	581	PheAspGly1leAlaThrGlyTyrLeuValLeuLysGluLeuGly1leLysValGlyLys 600
중 원	601	TyrvalAlaSerGluValCysGluGluSerIleAlaValGlyThrValLysHisGluGly 620
ठे व	621	AsnileLysTyrValAsnAspValArgAsnileThrLysLysAsnileGluGluTrpGly 640
8 8 8	64	660
දු දු	66	6—F
상 원	681	TyrSerArgProLysGluGlyAspAspArgProPhePheTrpMetPheGluAsnValVal 700
දු දු	701	AlametLysValGlyAspLysArgAspIleSerArgPheLeuGluCysAsnProValMet 720
9 8	L 4	0-0
ò	741	760
අ _ධ ,	2275	22
දු දු	761	GluTyrAenArgileAlaLysLysLysValGlnThrileThrThrLysSerAenSer 780
ò	78	leLysGlnGlyLysAsnGlnLeuPheProValValMetAsnGlyLysGluAspValLeu 800
Dp	2283	2283
ò i	80	uGluargilePheGlyPheProValHisTyrThraspValSerAsn 820
d D	2284	23
<u>ک</u> ۾	821	MetGlyArgGlyAlaArgGlnLysLeuLeuGlyArgSerTrpSerValProVal1leArg 840
ò	841	HisLeuPheAlaProLeuLysAspTyrPheAlaCysGlu 853

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Xie, S., Okano, M., and Li, E.

S Xie, S., Okano, M., and Li, E.

Direct Submission

L Submitted (28-MAY-1998) CVRC, Mass. Gen. Hospital, 149 13th Street,
Charlestown, MA 02129, USA

S Okano, M., Chijiwa, T., Sasaki, H. and Li, E.

Direct Submission

L Submitted (04-NOV-1999) CVRC, Mass. Gen. Hospital, 149 13th Street,
Charlestown, MA 02129, USA

Sequence update by submitter
On Nov 18, 1999 this sequence version replaced gi:3327979.

Location/Qualifiers

Incet
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/godon_start=1
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FHPLEGGLCOSCRRFTELETYNKOPVURKSKVRRSDSRNLEPREP
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NGTBLLNYTRPKGGNRFPFMMFBNVVANKNUNGKANSTRURGRSNSVPVIRHLFAPLKDYP
NGTBLLNYTRPKGGNRFPFMMFBNVVANKNUNGKANSTRURGRSNSVPVIRHLFAPLKDYP
NGTBLLNYTRPKGGNRFPMANTSVNNGNUNGRGRRGRSNSVPVIRHLFAPLKDYP
NGTBLDVLVGGRSNSVPVIRTERAPLENTYRDVSNMGRGRRGRSNSVPVIRTERFAPLKDYP
NGTBLDVLVGGRSNSVPVIRTERFAPLYTDVSNMGRGRRGRSNSVPVIRTERFAPLKDYP
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NGTRURGRSNSVPVIRTERFAPLYTDVSNMGRGRRGRSNSVPVIRTERFAPLYDVP
                                                             AF068626 4195 bp mRNA linear ROD 06-DEC-1999
Mus musculus DNA cytosine-5 methyltransferase 3B1 (Dnmt3b) mRNA,
alternatively spliced, complete cds.
                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus, 1 (bases 1 to 4128) to 1.00 Cokano, M. Xie, S. and Li, E. Cloning and characterization of a family of novel mammalian DNA (cytosine-5) methyltransferases (cytosine-1) methyltransferases 98324766
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Jeane="Dnmt3b"

/gene="Dnmt3b"

/note="similar to EST sequences deposited in GenBank

Ad407106, and AAS75617"

269. .2848
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/db_xref="taxon:10090"
/chromosome="2"
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                                                                                                                                                                 GlnValGluAlaAspSerGlyAspGlyAspSerSerGluTyrGlnAspGlyLysGluPhe
                                                                                                                                                                                                                           SerSerThrProTyrAlaArgLeuAlaGlnAspSerGlnGlnGlyGlyMetGluSerPro
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                                                                                                                                                                                                                                                                                                        ArgSerLeuArgArgAlaThrAlaSerAlaGlyThrProTrpProSerProProSer 163
                                                                                                                                                                                                                                                                              SerTyrLeuThrI1eAspLeuThrAspAspThrGluAspThrHisGlyThrProGlnSer
                                                                                                                                                                                                                                                                                                                                                      MetProLysLeuPheArgGlu------ThrArgThrArgSerGluSerProAlaVal 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrGlyAspGlyAspGly------GluAspGlyAspGlySerAspThrProVal 86
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SerGlnHisPheAsnLeuAlaThrPheAsnLysLeuValSerTyrArgLysAlaMetTyr 303
                                     PheGlyAspGlyLysPheSerGluValSerAlaAspLysLeuValAlaLeuGlyLeuPhe
                                                                                    ValSerTrpLysA1aThrSerLysArgGlnAlaMetSerGlyMetArgTrpVa1GlnTrp
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                                                                     GTGTCCTGGAAAGCCACCTCCAAGCGACAGGCCATGCCCGGAATGCGCTGGGTACAGTGG
                                                                                                                   GGAATAGGTGACCTCGTGTGGGGAAAGATCAAGGGCTTCTCCTGGTGGCCTGCCATGGTG
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643 AspLeuValIleGlyGlySerProCysAsnAspLeuSerAsnValAsnProAlaArgLys 662	γQ.
623 LysTyrValAsnAspValArgAsnIleThrLysLysAsnIleGluGluTrpGlyProPhe 6	B &
603 AlaSerGluValCysGluGluSerIleAlaValGlyThrValLysHisGluGlyAsnIle 6	94 70
583 GlylleAlaThrGlyTyrLeuValLeuLysGluLeuGlyIleLysValGlyLysTyrVal 6	B 8
563 LeuTyrProAlaIleProAlaAlaArgArgArgProIleArgValLeuSerLeuPheAsp 58 	β δ
544 ValArgLeuGlnAlaPhePheThrSerAspThrGlyLeuGluTyrGluAlaProLys 56	8 8
524 CYSTYYMOtCYSLeuProGlnArgCysHisGlyValLeuArgArgArgArgLysAspTrpAsn 54	유
504 LeuGluValLeuValGlyThrGlyThrAlaAlaGluAlaLysLeuGlnGluProTrpSer 52 	음 성
484 GlyArgGluLeuLeuCysSerAsnThrSerCysCysArgCysPheCysValGluCys 50 	유왕
464 GluLeuPheTyrMetTyrAspAspAspGlyTyrGlnSerTyrCysThrValCysCysGlu 48	유 성
444 ValSerPheHisProLeuPheGluGlyGlyLeuCysGlnThrCysArgAspArgPheLeu 46	상 생.
424 ValAlaAsnAsnLysSerSerLeuGluAspGlyCysLeuSerCysGlyArgLysAsnPro 44	음 <i>성</i>
404 TyrasnasnGlyLysaspargGlyaspGluaspGlnserargGluGlnMetalaSerasp 42	음 성
384 AlaAspAspSerAlaThrSerAspTyrCysProAlaProLysArgLeuLysThrAsnCys 40 :::	용. 성
364 ArgAlaGlySerArgLysLeuGluSerArgLysTyrGluAsnLysThrArgArgArgThr 383	B 8
344 GlyIleGluGlyLeuLysProAsnAsnThrGlnProValValAsnLysSerLysValArg 36 	음 성
324 SerLeuGluAspGlnLeuLysProMetLeuGluTrpAlaHisGlyGlyPheLysProThr 34 	음 성
304 HisAlaLeuGluLysAlaArgValArgAlaGlyLysThrPheProSerSerProGlyAsp 32 	음 성
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                                                                                                                                                               product="DNA cytosine-specific methyltransferase isoform
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                                                                                                              /function="methylates cytosine in DNA"
/note="alternatively spliced"
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Conservative:
Mismatches:
Indels:
/dev_stage="8-9 day old embryo"
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Mus musculus DNA cytosine-specific methyltransferase isoform 5
(Dnmrab) mRNA, complete cds.
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Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
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Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and Shen, Y.
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Thin B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
Shan. Y.
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                                            2452
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                                                                                                                                 683 ArgProLysGluGlyAspAspArgProPhePheTrpMetPheGluAsnValValAlaMet
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/organism="Mus musculus"
/strain="KM"
/db_xref="taxon:10090"
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AUTHORS
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roTrpSer 523	LeuGluValLeuValGlyThrGlyThrAlaAlaGluAlaLysLeuGlnGluPr	504	ફ
GGAGTGT 18	CCGTGAACTGCTGTGCAGTAACACAAGCTGCTGCAGATGCTTCTGTGT	1761	Db
alGluCy	yArgGluLeuLeuCysSerAsnThrSerCysCysArgCysPheCysVa	484	Ş
CTGTGAG 17	TATCAGTCCTACTGCACCGTGTC		망
scysG1	uLeuPheTyrMetTyrAspAspAspGlyTyrGlnSerTyrCysThrValCy	464	ફ
rgPheLeu 463	SerPheHisProLeuPheGluGlyGlyLeuCysGlnThrCysArgAspA :::	444 1641	유 성
GAACCCT 16			망
rabanDro 443	lAlaAsnAsnLvsSerSerLeuGluAsnGlvCvsLeuSerCvsGlvArgLu	4	Ş
laSerAsp 423 ::: CTTCTGAA 1580	rArgGluGlnMetAl ::: CCGAGAACGGATGGO	1524	음 성
rage 15	DAATGACTCTGCTGCTTCTGAGTCCCCCCCACCCAAGCGCC		ĝ
nCys 4	AspAspSerAlaThrSerAspTyrCysProAl :::	384	ઇ
GCACA 14	FICAGACAGTAGGAACTTAGAACCCAGGAGACG	0	뮍
ArqThr 38	laGlySerArgLysLeuGluSerArgLysTyrGluAsnLysThrArqAn	364	S
/sValArg 363 AGGTGCGT 1406	leGluGlyLeuLysProAsnAsnThrGlnProValValAsnLysSerLy CGAGGGCCTCAAACCCAACAAGAAGCAACCAGTGGTTAATAAGTCGAA	344 1347	용 성
CCTACT 13	TGGAGGACCAGCTGAAGCCCATGCTGGAGTGGGCCCACGGTGGCTTCAL	00 (당 .
ProThr 34	erLeuGluAspGlnLeuLysProMetLeuGluTrpAlaHisGlvGlvPheI	324	Ş
ProGlyAsp 323 ::: CTGGAGAG 1286	HisAlaLeuGluLysAlaArgValArgAlaGlyLysThrPheProSerSerPro	304 1227	유 성
laMetTyr 303 CATGTAC 1226	rGlnHisPheAsnLeuAlaThrPheAsnLysLeuValSerTyrArgLysAl 	284 1167	유 성
GCTGTTC 11	GTGATGCAAGTTTTCTGAGATCTCTGCTGACAAACTGGTGGCTCTGGC	0	В
YLeuPhe 28	spLysLeuValAlaLeuGl	264	γQ
	rLysargGlnalaMetSerGlyMetArgTrpVa caagcgacaggccaTgcccggaaTgcgcTgggT	44 47	B 8
laMetVal 243 CATGGTG 1046	;pG1yLys11eLysG1 	7	B OA
GAGTTT 9		927	용
Gluphe 22	SerGlyAspG	24	ş
luserPro 203 ::::: ATACCACA 926	erThrProTyrAlaArgLeuAlaGlnAspSerGlnGlnGlyGlyMetG 	84 67	음 성
TAAG	GACTTCATGGAAGAAGTGACAC	4	В
GlnSer 1	AspLeuThrAspAspThrGluAspThrHisGlyThrF	4.	Ş
GCCAGC 83	CGAGCATCGTCTTCAGCAAGCACGCCATGGTCATCCCC	7.4	B .
oProSe	gSerLeuArgArgArgAlaThrAlaSerAlaGlyThrProTrpProSerPr	144	Ş

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        ROD 08-JUN-2000
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Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
P.R.China
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product="DNA cytosine-specific methyltransferase isoform
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Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 4338)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
Shen, Y.
                                                                                                                                                                                                                                                                                                        Cloning of full-length Dnmt3b cDNA and its alternative splicing isoforms in mouse embryonic tissue Unpublished
AF151969 4338 bp mRNA linear ROD 08-JUN-
Mus musculus DNA cytosine-specific methyltransferase isoform 1
(Dnuralb) mRNA, complete cds,
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(note="alternatively spliced"
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Mismatches:
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/db_xref="taxon:10090"
/dev_stage="8-9 day old embryo"
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                                                                                                                                                                                               Sequence update by submitter
On Nov 18, 1999 this sequence
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                 Submitted (28-MAY-1998) CVRC,
Charlestown, MA 02129, USA
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                                                                                                                                                                                                                                                                                 Charlestown, MA 02129, USA 3 (bases 1 to 4135) Okano, M., Chijiwa, T., Sasaki, H.
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Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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1048 c 1106 g 938 t
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US-09-720-086-8 (1-853) x AF151974 (1-4163)
                                         IleLeuValAsnGlyAlaCysSerAspGlnSerSerAsp---
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ATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACACGAAGGATGCTCCCTCACCC
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Yin,B., Chen,Y.T., Zhu,M., Luo,Y.J., Zhu,N., Xu,S.C., Wu,G.Y. and Shen,Y.
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Biology, Institution of
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SEISADKLVALGLFSQHFULATFNKLVSYRKAMYHTLEKARVRAGKTFSSSPGESLED
QLKPMLEWAHGGFKPTGIEGLKPNKKQPENKSRRRTTNDSAASESPPFKLKTNSYGG
KDRGEDEESRERMASEVTUNKGNLEDRCLSCGKKNPVSFHPLFEGGLQSCCDRFFLEL
FYMYDEDGYQSYCTVCCEGRELLLCSNTSCCRCFCVECLEVLVGAGTAEDAKLQEPWS
CYMCLPQRCHGVLRRKDWNMRLQDFFTTDPDLEEFEPFKLYPAIPAAKRRPIRVLSL
FDGIATGYLVLKELGIKVEKYIASEVCAESIAVCTVKHEGOIKYVNDVRKITKKNIEE
WGPFDLVIGGSPCNDLSNVNPAAKKGLYEGTGRLFFEFYHGGILKYVNDVRKITKKNIEE
EMVYAMKVNDKKDISRELACNPVMIDAIKVSAAHRARYFWGNLPGMNRFVMASKNDKL
ELQDCLEFSRTAKLKKVQTITTKSNSIRQGKNQLFPVMNGKDDVLWCTELERIFGFP
ANYTDVSNNGRGARQKLLGRSWSVFVIRHLFAFLKDYFACE"
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AICTEPVCTPETRGRRSSSRLSKREVSSLLNYTQDMTGDGDRDDEVDDGNGSDILMPK
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1901 GCCCCAAGGAGGGGACAACGTCCATTCTTCTGGATGTTCGAGAATGTTGGCCATG 2360 1407 ACCAATGACTCTGCTGCTTCTGAG---TCCCCCCACCCAAGGGGCCTCAAGACAATAGC 1463 543 602 404 TyrAsnAsnGlyLysAspArgGlyAspGluAspGlnSerArgGluGlnMetAlaSerAsp 423 643 AspLeuValileGlyGlySerProCysAsnAspLeuSerAsnValAsnProAlaArgLys 662 484 GlyArgGluLeuLeuLeuCysSerAsnThrSerCysCysArgCysPheCysValGluCys 623 LysTyrValAsnAspValArgAsnIleThrLysLysAsnIleGluGluTrpGlyProPhe 424 ValAlaAsnAsnLysSerSerLeuGluAspGlyCysLeuSerCysGlyArgLysAsnPro 504 LeuGluValLeuValGlyThrGlyThrAlaAlaGluAlaLysLeuGlnGluProTrpSer 524 CysTyrMetCysLeuProGlnArgCysHisGlyValLeuArgArgArgLysAspTrpAsn 563 LeuTyrProAlaIleProAlaAlaArgArgArgProIleArgValLeuSerLeuPheAsp 583 GlyIleAlaThrGlyTyrLeuValLeuLysGluLeuGlyIleLysValGlyLysTyrVal 603 AlaSerGluValCysGluGluSerIleAlaValGlyThrValLysHisGluGlyAsnIle 663 GlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrHisLeuLeuAsnTyrSer LysValGlyAspLysArgAspIleSerArgPheLeuGluCysAsnProValMetIleAsp 544 ValArgLeuGlnAlaPhePheThrSerAspThrGlyLeu---GluTyrGluAlaProLys 703 g g g S ద g S qq q g da ð qq ò g ò 셤 ò ò 8 8 8 ò ò ò qq ò g ò ò

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Mammalia; Eutheria; R
1 (bases 1 to 4278)
Yin,B., Chen,Y.T., Zh
                                                                                                                                                                                                                                                                                                                                             Submitted (17-MAY-1999) Department of Biochemistry and Molecular Biology, Institution of Basic Medical Sciences, Chinese Academy Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning of full-length Dnmt3b cDNA and
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                                                                                                                                           /product="DNA 2"
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                                                /translation="MKGDSRHLNEEEGASGYEECIIVNGNFSDQSSDTKDAPSPPVLE
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SRRRRASSSASTPWSSPASVDFMEEVTPKSVSTPSVDLSQDGDQBGMDTTQVDAESIY
GDSTEVJDDKEFGIGDLVWGKIKGFSWWPAMVVSWKATSKRQAMPGMRWVQWFGDGKF
             SEISADKLVALGLFSQHFNLATFNKLVSYRKAMYHTLEKARVRAGKTFSSSPGESLED
QLKPMLEWAHGGFKPTGIEGLKPNKKQPENKSRRRTTNDSAASESPPPKRLKTNSYGG
KDRGEDEESRERMASEVTNNKGNLEDRCLSCGKKNPVSFHPLFEGGLCQSCRDRFLEL
FYMYDEDGYQSYCTVCCEGRELLLCSNTSCCRCFCVECLEVLVGAGTAEDAKLQEPWS
                                                                                                                  /protein_id="AAF74516.1"
/db_xref="GI:8347120"
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'note="alternatively spliced"
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CYMCLPQRCHGVLRRRKDWNWRLQDFFTTDPDLEEFEPYKLYPAIPAAKRRPIRVLSLFDGIATGYLVLKELGIKVEKYIASEVCAESIAVGTVKHEGQIKYVNDVRKITKKNIEE WGFFDLVIGGSPCNDLSNVNPARKGLYEGTGRLFFEFYHLNYTRPKEGDNRPFWMFENVVAMKVNDKKDISRFLACNPVMIDAIKVSAAHRARYFWGNLPGMNRPVMASKNDKLELQCLLEFSRTAKLKKVQTITTKSNSIRQGKNQLFPVVMNGKDDVLWCTELERIFGFPAHYTDVSNMGRGARQKLLGRSWSVPVIRHLFAPLKDYFACE"

US-09-720-086-8 (1-853) Percent Similarity: GTCAGTACCCCATCAGTTGACTTGAGCCAGGATGGAGATCAGGAGGGTATGGATACCACA GlyIleGlyAspLeuValTrpGlyLysIleLysGlyPheSerTrpTrpProAlaMetVal GlnValGluAlaAspSerGlyAspGlyAspSerSerGluTyrGlnAspGlyLysGluPhe ATTATCGTTAATGGGAACTTCAGTGACCAGTCCTCAGACACGAAGGATGCTCCCTCACCC ValSerTrpLysAlaThrSerLysArgGlnAlaMetSerGlyMetArgTrpValGlnTrp SerSerThrProTyrAlaArgLeuAlaGlnAspSerGlnGlnGlyGlyMetGluSerPro SerSerSerArgLeuSerLysArgGluValSerSerLeuLeuSerTyrThrGlnAspLeu IleLeuValAsnGlyAlaCysSerAspGlnSerSerAsp------ATGAAGGGAGACAGCAGCATCTGAATGAAGAAGAGGGTGCCAGCGGGTATGAGGAGTGC MetLysGlyAspThrArgHisLeuAsnGlyGluGluAspAlaGlyGlyArgGluAspSer Scores: GGAATAGGTGACCTCGTGTGGGGAAAGATCAAGGGCTTCTCCTGGTGGCCTGCCATGGTG CAGGTGCATGCAGAGCATATATGGAGACAGCACAGAGTATCAGGATGATAAAGAGTTT ------GTCGACTTCATGGAAGAAGTG---SerTyrLeuThrlleAspLeuThrAspAspThrGluAspThrHisGlyThrProGlnSer ArgSerLeuArgArgArgAlaThrAlaSerAlaGlyThrProTrpProSerProProSer ACCCGAGGTCGGCAGGGCCGCCACCATGTGCAGGAGTACCCTGTGGAGTTTCCGGCTACC ThrargGlyArgGlnGlyArgAsnHisValAspGluSerProValGluPheProAlaThr CGAACCCGACATAGCAATGGGACCTCCAGCTTGGAGAGGCCAAAGAGCCTCCCCCAGAATC ArgThrArgAsnAsnAsnSerValSerSerArgGluArgHisArgProSerProArgSer ATGCCAAAGCTCACCCGTGAGACCAAGGACACCAGGACGCGCTCTGAAAGCCCCGGCTGTC MetProLysLeuPheArgGlu----ACAGGAGATGGAGAGAGATGATGAAGTAGATGGGAATGGCTCTGATATT----CTA ThrGlyAspGlyAspGly-----TCAAGCTCCCGGCTGTCTAAGAGGGAGGTCTCCAGCCTTCTGAATTACACGCAGGACATG CCAGTCTTGGAGGCAATCTGCACAGAGCCAGTCTGCACACCAGAGACCAGAGGCCGCAGG ProlleLeuGluAlaIle------ArgThrProGluIleArgGlyArgArg AGGTCTCGGAGACGTCGAGCATCGTCTTCAGCAAGCACGCCATGGTCATCCCCTGCCAGC Similarity: 1055 Ð 5.01e-186 3664.00 86.68% 80.60% 80.25% x AF151970 (1-4278) ი ω Length: Matches: Conservative: Gaps: Mismatches: Indels: -GluaspGlyAspGlySeraspThrProVal -ThrArgThrArgSerGluSerProAlaVal -----ACACCTAAGAGC SerPro 243 1043 888 103 263 1101 223 203 981 183 948 163 143 828 123 768 708 86 651 70 591 50 531 35 471

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1636 GTCACCAACAACAAGGGCAATCTGGAAGACCGCTGTTTGTCCTGTGGAAGAAGAAGAACCCT 1695
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                                               1222 TTTGGTGATGGCAAGTTTTCTGAGATCTCTGCTGACAAACTGGTGGCTCTGGGGGCTGTTC 1281
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1162 GTGTCCTGGAAAGCCACCTCCAAGCGACAGGCCATGCCCGGAATGCGCTGGGTACAGTGG 1221
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                           PheGlyAspGlyLysPheSerGluValSerAlaAspLysLeuValAlaLeuGlyLeuPhe 283
                                                                                          284 SerGlnHisPheAsnLeuAlaThrPheAsnLysLeuValSerTyrArgLysAlaMetTyr 303
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4006 bp mRNA linear ROD 01-JUL-2002 Mus musculus DNA cytosine methyltransferase 3b6 (Dnmt3b6) mRNA, complete cds, alternatively spliced.
AX078427
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Chen, T., Udda, Y. and Li, E.
Dnmt3a2 encoded by transcripts from an intronic promoter of Dnmt3a is expressed abundantly in ES cells and germ cells
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Chen, T., Ueda, Y. and Li,E.
Direct Submission
Submitted (08-FEB-2002) Cardiovascular Research Center,
Massachusetts General Hospital, 149 13th Street, Charlestown, MA
02129, USA.
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623 LysTyrValAspValArgAsnIleThrLysLysAsnIleGluGluTrpGlyProPhe
                                                                               643 AspleuValileGlyGlySerProCysAsnAspLeuSerAsnValAsnProAlaArgLys
                                                                                                        2296 GACTTGGTGGTGGAAGCCCATGCAATGATCTCTCTAACGTCAATCTGTGGCCGGAAA
                                                                                                                                                                                                                                                                                                                                     703 LysvalGlyAspLysArgAsplleSerArgPheLeuGluCysAsnProValMetIleAsp
                                                                                                                                                                                                                                                                                                                                                                                                                         723 AlaileLysValSerAlaAlaHisArgAlaArgTyrPheTrpGlyAsnLeuProGlyMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           763 AsnArgIleAlaLysLeuLysLysValGlnThrIleThrThrLysSerAsnSerIleLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 803 ThrGluLeuGluArgIlePheGlyPheProValHisTyrThrAspValSerAsnMetGly
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                                                                                                                                                                   663 GlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrHisLeuLeuAsnTyrSer
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AICTEPVCTPETTGRRSSSRLSKREVGSLLNYTQDMTGDGDRDDEVDDGNGSDILMPK
LTRETKDTRTRSESPAVTRHSNGTGSLERQRASPRITRGRQGRHPVQEYPVEFPATR
SRRRRASSSASTPWSSPASVDFMEEVTPKSVSTPSVDLSQDGDOEGMDTTQVDAESRD
GDSTEYQDDKEFGIGDLVWGKIKGFSWWPAMVVSWKATSKRQAMPGMRWVQWFGDGKF
SEISADKLVALGLFSQHFWLATFNKLVSYRKAMYHTLEKARVRAGKTFSSSPGESLED
QLKPMLEWAHGGFFKPTGIEGLKPNKKQPVVNKSKVERSDSRNLEPRRRENKGRRRTTN
DSAASESPPFKRTGIGLKPNKKQPVVNKKVERVTNNKGNLEDRCLSCGKKNPVS
FHPLFEGGLCQSCRDRFLELFYMYDEDGYQSYCTVCCEGRELLLCSNTSCCRCFCVEC
LEVLVGAGTAEDAKLGEPWSCYMCLPQRCHGVLKELGIKVEKYLASEVCASIAVGTVKH
EGQIKYVNDVRKITKKNIEEWGPFDLVIGGSPCNDLSNVNPARKGLYEGTGRLFFEFY
HLLNYTRPKEGDNRFPFWMFENVVANKVNDKKDISRFLACNPYMIDAIKVBAAHRARY
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/strain="12984/SvJae"
/db_xref="taxon:10090"
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/product="DNA cytosine methyltransferase
/protein_id="AAL85481.1"
/db_xref="GI:21655121"
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                                                                      GAGCTCTTCTACATGTATGATGAGGACGGCTATCAGTCCTACTGCACCGTGTGCTGTGAG
                                                                                                                                                         GTGTCCTTCCACCCCCTCTTTGAGGGTGGGCTCTGTCAGAGTTGCCGGGATCGCTTCCTA
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                                           LysTyrvalAsnAspValArgAsnIleThrLysLysAsnIleGluGluTrpGlyProPhe
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                           504 LeuGluValLeuValGlyThrGlyThrAlaAlaGluAlaLyBLeuGlnGluProTrpSer
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/ Canalarion="WKGDSRHINBEEGASGYBECIIVNGNFSDQSSDTKDAPSPPY
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Yin, B., Chen, Y. T., Zhu, M., Luo, Y. J., Zhu, N., Xu, S.C., Wu, G. Y. and
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2 (bases 1 to 4034)
Yin,B., Chen,Y.T., Zhu,M., Luo,Y.J., Zhu,N., Xu,S.C., Wu,G.Y. and Shen,Y.
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297. . 2687
/gene="Dnmt3b"
/function="methylates cytosine in DNA"
/note="alternatively spliced"
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Conservative:
Mismatches:
Indels:
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/dev_stage="8-9 day old embryo"
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AF151975.1 GI:8347134
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23	204 GlnValGluAlaAspSerGlyAspGlyAspSerSerGluTyrGlnAspGlyLysGluPhe 2	음 성
03	184 SerSerThrProTyrAlaArgLeuAlaGlnAepSerGlnGlnGlyGlyMetGluSerPro 2	B 8
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73	alGluPheProAlaThr 1	S S S
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03 53	MetProLysLeuPheArgGluThrArgThrArgSerGluSerProAlaVal 1	용 성
93 6	lySerAspThrProVal 8 CTCTGATATTCTA 5	_B &
36	SerSerSerArgLeuSerLysArgGluValSerSerLeuLeuSerTyrThrGlnAspLeu 7	용왕
0 76	LeuGluAlaIleArgThrProGluIleArgGlyArgArg 5 	무양
5 16	euValAsnGlyAlaCysSerAspGlnSerSerAspSerPro 3 ::	P 9
56	7 ATGAAGGGAGACAGCAGACATCTGAATGAAGAAGAGGGTGCCAGCGGGTATGAGGAGTGC 3	뫄

722 2480	703 LysValGlyAspLysArgAspIleSerArgPheLeuGluCysAsnProValMetIleAsp	라 성
702 2420	683 ArgProLysGluGlyAspAspArgProPhePheTrpMetPheGluAsnValValAlaMet	B 8
682 2360	heTyrHisLeuLeu! TTACCACTTGCTG!	g dy
662 2300	643 AspLeuVallleGlyGlySerProCysAsnAspLeuSerAsnValAsnProAlaArgLys	dg Vo
642 2240	pValArgAsnIleGl 	P 6
622 2180	03 AlaSerGluValCysGluGluSerIleAlaValGlyThrValLy,	4G 4D
602 2120	83 GlyIleAlaThrGlyTyrLeuValLeuLysGluLeuGlyIleLysValGlyLysTyr 	유 <i>칭</i>
582 2060	563 LeuTyrProAlaileProAlaAlaArgArgArgProIleArgValLeuSerLeuPheAsp	p
562 2000	544 ValArgLeuGlnAlaPhePheThrSerAspThrGlyLeuGluTyrGluAlaProLys	B 8
543 1940	524 CysTyrMetCysLeuProGlnArgCysHisGlyValLeuArgArgArgAysAspTrpAsn 	B &
523 1880	504 LeuGluValLeuValGlyThrGlyThrAlaAlaGluAlaLysLeuGlnGluProTrpSer 	99 Q y
503 1820	484 GlyArgGluLeuLeuCysSerAsnThrSerCysCysArgCysPheCysValGluCys	B 64
483 1760	464 GluLeuPheTyrAspAspAspAspGlyTyrGlnSerTyrCysThrValCysCysGlu 	당 &
463 1700	444 ValSerPheHisProLeuPheGluGlyGlyLeuCysGlnThrCysArgAspArgPheLeu	B 8
443 1640	424 ValAlaAsnAsnLysSerSerLeuGluAspGlyCysLeuSerCysGlyArgLysAsnPro	90 VQ
423 1580	404 TyrAsnAsnGlyLysAspArgGlyAspGluAspGlnSerArgGluGlnMetAlaSerAsp	g 29
	84 ALAASDARDSERALATINISERASDTYTCYSEPTOALAPTOLYSATGLEULYSTINIASTICY = ::	g 4
00 44 (64 ArgAlaGlySerArgLysLeuGluSerArgLysTyrGluAsnLysThrArgArgArgTh :::	b b

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4149 bp mRNA linear ROD 08-JUN-2000 Mus musculus DNA cytosine-specific methyltransferase isoform 4 (Dnnmi3b) mRNA, complete cds.
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|db_xref="G1:8347126"
|/tb_xranslation="MKGDRFHIANEBGASGYEECIIVNGNFSDQSSDTKDAPSPPVLE
|/translation="MKGDRFHIANEBGASGYEECIIVNGNFSDQSSDTKDAPSPPVLE
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/product="DNA cytosine-specific methyltransferase isoform
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Yii, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and June B. C. Chen, Y.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cloning of full-length Dnmt3b cDNA and its alternative splicing isoforms in mouse embryonic tissue Unpublished
                     2481 GCCATCAAGGTGTCTGCTGCTCACAGGCCCCGGTACTTCTGGGGTAACCTACCGGAATG 2540
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                                                                                                                                                     763 AsnArgIleAlaLysLeuLysLysValGlnThrIleThrThrLysSerAsnSerIleLys 782
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723 AlaileLysvalSerAlaAlaHisArgAlaArgTyrPheTrpGlyAsnLeuProGlyMet
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note="alternatively spliced"
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/dev_stage="8-9 day old embryo"
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                                  LeuTyrProAlaIleProAlaAlaArgArgArgProIleArgValLeuSerLeuPheAsp
                                                                                          ValArgLeuGlnAlaPhePheThrSerAspThrGlyLeu---GluTyrGluAlaProLys
                                                                                                                                    CysTyrMetCysLeuProGlnArgCysHisGlyValLeuArgArgArgLysAspTrpAsn
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                                                                        ATGCGCCTGCAAGACTTCTTCACTACTGATCCTGACCTGGAAGAATTTGAGCCACCCAAG
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                                    Mus musculus.

Mus musculus

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 3946)

1 (bases 1 to 3946)

1 (bases 1 to 3946)
Okano,M., Xie,S. and Li,E.
Cloning and characterization of a
(cytosine-5) methyltransferases
Nat. Genet. 19 (3), 219-220 (1998)
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Mus musculus DNA cytosine-5 methyltransferase
alternatively spliced, complete cds.
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| region start=1 |
| product="DNA cytosine-5"methyltransferase 3B3" |
| product="DNA cytosine-5"methyltransferase 3B3" |
| product="DNA cytosine-5"methyltransferase 3B3" |
| product="1" id=#AAA(40180.2" |
| db xref="G1:6449474" |
| db xref="G1:6449474" |
| frānslation="MKGDSRHLNEEGASGYEECIIVNGNFSDQSSDTKDAPSPPVLE |
| frānslation="MKGDSRHLNEEGASGYEECIIVNGNFSDGSSDTKDAPSPSSTLMPK |
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                       So (250-5)
Xie, S., Okano, M. and Li, E.
Direct Submission

Submitted (28-MAY-1998) CVRC, Mass. Gen. Hospital, 149 13th Street, Charlestown, MA 02129, USA
3 (Bases I to 3946)
3 (Bases I to 3946)
Okano, M., Chijiwa, T., Sasaki, H. and Li, E.
Direct Submission
Submitted (04-NOV-1999) CVRC, Mass. Gen. Hospital, 149 13th Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="de novo DNA methylation"
/note="alternatively spliced product; contains Cys-rich
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Sequence update by submitter
On Nov 18, 1999 this sequence version replaced gi:3327983
Location/Qualifiers
1. 3946
/ Organism="Mus musculus"
/ db xref="taxon:10090"
/ chromosome="2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-MAY-1999) Department of Biochemistry and Molecular Biology, Institution of Basic Medical Sciences, Chinese Academy (Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cloning of full-length Dnmt3b cDNA isoforms in mouse embryonic tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 3974)
Yin,B., Chen,Y.T., Zhu,M., Luo,Y.J., Zhu,N., Xu,S.C.
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             GDSTEYQDDKEFG1GDLVWGK1KGFSWWPAMVVSWKATSKRQAMPGMRWVQWFGDGKF
SE1SADKLVALGLFSOHFNLATTWKLVSYRKAMYHTLEKARVRAGKTFSSSPGESLED
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CLKPMLEWAHGGFKPTG1EGLKPNKKOPENKSRRTTND3PFBPFRLLKTNNSYGG
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AICTEPVCTPETRGRRSSSRLSKREVSSLLNYTQDMTGDGDRDDEVDDGNGSDILMPK
LTRETKDTRTRSESPAVRTRHSNGTSSLERQRASPRITRGRQGRHHVQEYPVEFPATR
SRRRRASSSASTPMSSPASVDFMEEVTPKSVSTPSVDLSQDGDQEGMDTTQVDAESIY
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                                                                                                                                                                                        /protein_id="AAF74522.1"
/db_xref="GI:8347137"
                                                                                                                                                                                                                                                          /note="alternatively
/codon_start=1
                                                                                                                                                                                                                                                                                             /gene="Dnmt3b"
/function="methylates
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dev_stage="8-9 day olo
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상 원	y 1 MetlysGlyAspThrArgHisLeuAsnGlyGluGluAspAlaGlyGlyArgGluAspSer 	20 356
<u>ک</u> ۾	y 21 IleLeuValagnGlyalaCygSerAspGlnSerSerAspSerPro	35 416
<u>ئ</u> ۾	y 36 ProlleLeuGluAlaileArgThrProGluileArgGlyArgArg	50 476
දු පු	y 51 SerSerSerArgLeuSerLysArgGluValSerSerLeuLeuSerTyrThrGlnAspLeu	70 536
රු සි	y 71 ThrGlyAspGlyAspGlyGluAspGlyAspGlySerAspThrProVal	86 593
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දු පු	y 124 ThrArgGlyArgGlnGlyArgAsnHisValAspGluSerProValGluPheProAlaThr	143 773
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දු පු	y 164 SerTyrLeuThrIleAspLeuThrAspAspThrGluAspThrHisGlyThrProGlnSer	183 866
දු දු	y 184 SerSerThrProTyrAlaArgLeuAlaGlnAspSerGlnGlnGlnGlyMetGluSerPro	203
& g	y 204 GlnValGluAlaAspSerGlyAspGlyAspSerSerGluTyrGlnAspGlyLysGluPhe	223 986
è 8	y 224 Gly1leGlyAspLeuValTrpGlyLysIleLysGlyPheSerTrpTrpProAlaMetVal	243 1046
6 6	y 244 ValSerTrpLysAlaThrSerLysArgGlnAlaMetSerGlyMetArgTrpValGlnTrp	263
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                                                                                                                                                                                                                                                                                        743 AsnArgProValIleAlaSerLysAsnAspLysLeuGluLeuGlnAspCysLeuGluTyr 762
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                                                      CGCGGCGCCCGTCAGAAGCTGCTGGGCAGGTCCTGGAGTGTACCGGTCATCAGACACCTG 2591
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Search completed: November 22, 2002, 10:59:08 Job time : 4955.31 secs

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Command line parameters:

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-DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE+LOCAL
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-MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPDEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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38: em_sy:*
39: em_htg_o_mus:*
41: em_htgo_mus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 3005)

                                                                                                                                Wang, Z., Okano, M., Nogami, M., Li, Y., He, W.W., Okumura, K.
                                                                                                                                                 Cloning, expression and chromosome locations of the human DNMT3 gene family Gene 236 (1), 87-95 (1999)
                                                                                                                                                                                                                  Xie, S., Okano, M. and Li, E.

Direct Submission
Submitted (22-MAY-1998) CVRC, Mass. General Hospital, 149 13th
Street, Charlestown, MA 02129, USA
3 (bases 1 to 3005)
Hata, K., Shirohzu, H., Sasaki, H. and En, L.
Direct Submission
Street, Charlestown, MA 02129, USA
Street, Charlestown, MA 02129, USA
Squence update by submitter
On Feb 12, 2010 this sequence version replaced gi:4927369.
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290. 2968
/fene="DNMT3A"
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/product="DNA cytosine methyltransferase 3 alpha"
/protein_id="Aph33084_2"
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                                                   IleMetTyrValGlyAspValArgSerValThrGlnLysHisIleGlnGluTrpGlyPro
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TTCGATCTGGTGATTGGGGGCAGTCCCTGCAATGACCTCTCCATCGTCAACCCTGCTCGC
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4258)

Ni,J., Pradhan,S. and Roberts,R.J.

Cloning, expression and characterization of human DNMT3 genes
                                                                                                                                                           2 (bases 1 to 4258)
Ni,J., Pradhan,S. and Robert
Direct Submission
Submitted (22-DEC-2000) New
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WCTEMERVFGPPVHYTDVSNNSRLAARRSNSILGRSWSVPVIRHLFAARLYFACV"

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දු දු	321	AlaalagiugiyThrargTrpValMetTrpPheGlyAspGlyLysPheSerValValCys
දු දි	341	ValGluLysLeuMetProLeuSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsn
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& &	401	ValginasniysPrometilegiuTrpalaleuGiyGiyPheginProSerGiyProLys
≱ g	421	GlyLeuGluProproGluGluGluLysasnProTyrLysGluValTyrThraspMetTrp
y da	441	ValgluprogludladladladjatyralaproproproprodlabysLysProdrgbysSer
<u>ک</u> ۾	461 1598	Thralagiulysprolysvallysgiuiletieabgiuargthrarggiuargleuval
& 8	481	TyrGluValArgGlnLysGysArgAsnIleGluAspIleCysIleSerCysGlySerLeu
& 8 €	501	AsnValThrLeuGluHisProLeuPheValGlyGlyMetCysGlnAsnCysLysAsnCys
<u>ک</u> ۾	521	PheLeuGluCysAlaTyrGlnTyrAspAspAspGlyTyrGlnSerTyrCysThrIleCys
≿ 8	541	CysGlyGlyargGluValleuMetCysGlyAsnAsnAsnAsCysCysAArgCysPheCysVal
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                                                                                                        LeuPheAlaProLeuLysGluTyrPheAlaCysVal
                                                                                                                                                                     SerArgLeuAlaArgGlnArgLeuLeuGlyArgSerTrpSerValProValIleArgHis 900
                                                                                                                                                                                                                                  CysThrGluMetGluArgValPheGlyPheProValHisTyrThrAspValSerAsnMet
                                                                                                                                                                                                                                                                                             LysGlnGlyLysAspGlnHisPheProValPheMetAsnGluLysGluAspIleLeuTrp 860
                                                                                                                                                                                                                                                                                                                                                        HisGlyArgIleAlaLysPheSerLysValArgThrIleThrThrArgSerAsnSerIle
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Percent Similarity:
Best Local Similarity:
Query Match:

1.26e-180 4740.50 97.15% 96.27% 96.06%

> Matches: Conservative: Mismatches: Indels:

4192 877 8 25

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AF068625.2
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Submitted (04-NOV-1999) CVRC,
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Direct Submission
Submitted (28-MAY-1998) CVRC,
Charlestown, MA 02129, USA
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Cloning and characterization of a family
(cytosine-5) methyltransferases
Nat Canat 10 (2) 216 226 (2)
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Okano, M., Chijiwa, T., Sasaki, H. and Li, E
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Mammalia; Eutheria;
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                                                                     VGRPGREKKHPPVESSDTPKDPAVTTKSQPMAQDSGPSDLLPNGDLEKKSEPQPEEGS
PAAGQKGAPAEGECTETPPEASBRAVENGCCVTKEGRASAGEGKEQKQTNJESMKME
GSRGRLRGGLGWESSLRQR PMPALPQAGDPYY IS KRKDEWLARWKEAAEKKAKVIA
VMNAVEERQASGESQKVEEAS PPAVQQPTDPASETVATTPEPVGGDAGDKNATKAADD
EPEYEDGRGFGIGELVWGKLRGFSWWPGRIVSWWMTGRSRAAEGTRWVMWFGDCKFSV
VCVEKLMPLSSFCSAFHQATYNKQDMYRKAIYEVLQVXASSRACKLFPACHLDSDESDSG
KAVEVQNKOMIEWALAGGFQPSGFKGLEPPEEEKNPYKEVYTDMWVEPEAAAAYAPPPPA
KKPRKSTTEKPKVKEIIDERTRERLYEVENQKCRNIEDICISCGSLNVTLEHPLFIGG
MCQNCKNCFLECAYQYDDDGYQSYCTICCGGREVLMCGNNNCCRCFCVECVDLLVGPG
AQQAAIKEDPWNCYMCGHKGTYGLLRRREDWPSRLQMFFANNHDQEFDPKKYYPPVPA
EKRKPIRVLSLFDGIATGLLVLKDLGIQVDRYIASEVCEDSITVGMYRHQGKNTVYGD
VRSVTQKHIQEWGPFDLVIGGSPCNDLSIVNPARKGLYEGTGSLFFEFYRLHDARPK
EGDDRPFFWLFENVVAMGVSDKRDISRFLESNPVNIDAKEVSAAHRARYFWGNLPGMN
RPLASTYNDKLELQECLEHGRIAKESKVRTITTRSNSIKGGKDQHFPVFMMEKEDILW
RPLASTYNDKLELQECLEHGRIAKESKVRTITTRSNSIKGGKDQHFPVFMMEKEDILW
RPLASTYNDKLELQECLEHGRIAKESKVRTITTRSNSIKGGKDQHFPVFMMEKEDILW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to EST sequences deposited in GenBank Accession Numbers AA052791, AA1111043, AA154890, AA240794, AA756653, W58898, W59299, W91664, and W91665"
                                                    CTEMERVFGF PVHYTDVSNMSRLARQRLLGRSWSVPVIRHLFAPLKEYFACV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="DNA cytosine-5
/protein_id="AAC40177.2"
/db_xref="GI:6449468"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function="de novo DNA methylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="Dnmt3a"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MPSSGPGDTSSSSLEREDDRKEGEEQEENRGKEERQEPSATARK
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6666666	142 GlyArgGlyAlaProAlaGluAlaGlyLysGluGlnLysGluThrAsnIleGluSerMet 161
6 6 6 6 6	02 LysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGluLysLysAlaLysValile 2 I
6 6 6 6 6 6 6 6 6	262 ProGluProValGlySerAspAlaGlyAspLyaAsnAlaThrLyaAlaGlyAspAspGlu 281 988 CCTGAGCCAGTAGGAGGGGACAGGACGGACGATGAG 282 CCTGAGCCAGTAGGAGGGGACAGGACGCCAAGGAGCCGAGGATGAG 1048 CCTGAGTATGAGGATGGCGGGGCTTTGAGATGCTGGGGGGAAACTTCGG 1107 302 GlyPheSerTrpTrpProGlyArg1leValSerTrpTrpMetThrGlyArgSerArgAla 321 1108 GGCTTCTCCTGGTGGCGGGCCTTTGGCATTGGAGGAGGAGGAAACTTCGG 1107 322 AlaGluGlyThrArgTrpValMetTrpPheGlyAspGGTGGGAGGCGGAGCCGAGCA 1167 324 AlaGluGlyThrArgTrpValMetTrpPheGlyAspGGTGAGGAGGGGGGGCGAGCA 1167 325 AlaGluGlyThrArgTrpValMetTrpPheGlyAspGGTGAGGAGGGGAGCGGAGCCGAGCA 1167 326 GGTGAAGGCCTCGCTGGGTCATGTGGTTCTCGGAGATGGCAAGTGTGTGT

q _Q	1228	GAGAAGCTCATGCCGCTGAGCTCCTTCTGCAGTGCATTCCACCAGGCCACCTACAAGAAG 1287
\$ 8 8	362	GINPROMECTYAREQUEAGAIAINETYTGIUVAILENGINVAIAASERSERARGAIAGIY 381
ò	382	LysLeuPheProValCysHisAspSerAspGluSerAspThrAlaLysAlaValGluVal 401
QQ	1348	AAGCTGTTTCCAGCCTTGCCATGACAGTGATGAAAGTGACAGTGGCAAGGCTGTGGGAAGTG 1407
& 43	402	402 GlnasnLysProMetIleGluTrpAlaLeuGlyGlyPheGlnProSerGlyProLygGly 421
ò	422	LeuGluProProGluGluGluLysAsnProTyrLysGluValTyrThrAspMetTrpVal 441
Q O	1468	CTGGAGCCACCAGAAGAAGAAGAATCCTTACAAGGAAGTTTACACCGACATGTGGGTG 1527
ò 8	1528	GlubroGlublahlahlaryrAllabrobrobroblalysiysbrohrgiysserthr 461
ò	462	AlaGluLysProLysValLysGluIleIleAspGluArgThrArgGluArgLeuValTyr 481
gr	9 9 1	ACAGAGAAACCIAAGGICAAGGAICATIGATGAGCGCACAAGGGGGCGCTGGTGTAT 1647
Š 8	482	Gludar Argdin Lystyskrafasni Legluda piletysi Lesertysty yserkeudan 501
જે ઇ	502	ValThrLeuGluHisProLeuPheValGlyGlyMetCysGlnAsnCysBysAsnCysPhe 521
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ò	542	GlyGlyArgGluValLeuMetCygGlyAsnAsnAsnCysCygArgCygPheCygValGlu 561
Q (878	GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
S d	562 1888	CybvalAspLeuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLybGluAspProTrp 581
ò	582	AsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLeuLeuArgArgArgGluAspTrp 601
qa	1948	AACTGCTACATGTGCGGGCATAAGGGCACCTATGGGCTGCTGCGAAGACGGGAAGACTGG 2007
ò	602	ProSerArgLeuGlnMetPhePheAlaAsnAsnHisAspGlnGluPheAspProProLys 621
qq	2008	CCTTCTCGACTCCAGATGTTCTTTGCCAATAACCATGACCAGGAATTTGACCCCCAAAG 2067
ò £	622	ValTyrProProValProAlaGluLysArgLysProIleArgValLeuSerLeuPheAsp 641
ò	642	Glv1leAlaThrGlvLeuLeuValleuLvaAsnLeuGlv1leGlnVallanardTvr1le 661
6 A	2128	GGGATTGCTACAGGGCTCCTGGTGCTGAGGACCTGGGCATCCAAGTGGACGCTACATT 2187
È	662	AlaSerGluValCysGluAspSerIleThrValGlyMetValArgHisGlnGlyLysIle 681
ag	2188	GCCTCCGAGGTGTGTGAGGACTCCATCACGGTGGGGTGG
රි සි	682	MettyrvalGlyAspValArgSerValThrGlnLy8HisIleGlnGluTrpGlyProPhe 701
è	702	AsnienVallleGlvGlvGarProCvsAsnAsnienSertleValasnDroblasertvo 721
g qg	2308	GACCTGGTGATTGGAGGCAGTCCCTGCAATGACCTCTCCATTGTCAACCCTGCCCGCAAG 2367

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                                                                                          CDNA
                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                 Direct Submission

Direct Submission

Submitted (01-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11AO3, Bethesda, MD 20892-2590,
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Mammalia; Eutheria; Rodentia;
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                    Contact:
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             A Library Preparation: Life Technologies, Inc.
A Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: Sequencing Group at the Stanford Human
ter, Stanford University School of Medicine, Stanford,
site: http://www-shgc.stanford.edu
teact: (Dickson, Mark) mcd@paxil.stanford.edu
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Grimwood, J., Rodriquez,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MPSSGFGDTSSSSLEREDDRKEGEEQEENRGKEERQEPSATARK
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VRSVTQKHIQEWGPFDLVIGGSPCNDLSIVNPARKGLYEGTGRLFFEFYRLLHDARPK
EGDDRPFWLFENVLANGVSDKRDISRFLESNPWIDAKEVSDAHRARYFWGMLFGMN
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CTEMERVFGFPVHYTDVSNMSRLARQRLLGRSWSVPVIRHLFAPLKEYFACV"
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/protein_id="AAH07466.1"
/db_xref="GI:13938621"
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/lab_host="DH10B"
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arose spontaneously from a senescent normal mammar
(clonal) outgrowth infected with the virus MMTV."
(clonelib="MCI_CGAP_Lu29"
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/db_xref="razon:10090"
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—ფ	4 5	142 GlyArgGlyAlaProAlaGluAlaGlyLySGluGlnLySGluThrAsnileGluSerMet 161 	62 LysMetGluGlySerArgGlyArgLeuArgGlyGlyLeuGlyTrpGluSerSerLeuArg 18	0 17 0	202 LysargaspGluTrpLeualaargTrpLysargGlualaGluLysLysalaLysVal11e 221 	222 AlaGlyMetAsnAlaValGluGluAsnGlnGlyProGlyGluSerGlnLysValGluGlu 241 	242 AlaSerProProAlaValGInGInProThrAspProAlaSerProThrValAlaThrThr 261	262 ProgluProValglySerAspAlaglyAspLysAsnAlaThrLysAlaglyAspAspGlu 281 	yPheGlyIleGlyGluL cttrGGCATTGGAGAGC	302 GlyPheSerTrpTrpProGlyArg1leValSerTrpTrpMetThrGlyArgSerArgAla 321 	322 AlaGluGlyThrargTrpValMetTrpPheGlyAspGlyLy9PheSerValValCy9Val 341 	342 GlubysLeuMet ProLeuSerSerPheCysSerAlaPheHisGlnAlaThrTyrAsnLys 361 	162 GlnPrometTyrargLysalaileTyrGluValLeuGlnValAlaSerSerargAlaGly 181 	382 LysteuPheProValCysHisAspSerAspGluSerAspThrAlaLysAlaValGluVal 401	402 GlnAsnLysProMetIleGluTrpAlaLeuGlyGlyPheGlnProSerGlyProLysGly 421 	422 LeugluProProgluglugluLysAsnProTyrLysGluValTyrThrAspMetTrpVal 441 	442 GlubroGlualaalaalaayralabrobroProPloalaLysEysProArgLysSerThr 461 	462 AlaGluLysProLysValLysGlullelleAspGluArgThrArgGluArgLeuValTyr 481
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                                                                                                        Chen, G., Chen, R., Chewalny, J., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., Davis, C., Davy-Carroll, L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delyan-Rocha, S., Durbin, K.J., Falla, T., Ferraguto, D., Plagg, M., Ford, J., Escotto, M., Falla, T., Ferraguto, D., Plagg, M., Ford, J., Escotto, M., Falla, T., Ferraguto, D., Plagg, M., Ford, J., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hems, S.C., Harris, K., Hart, M., Holloway, C., Hollins, B., Jacobson, B., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Nea, P., Pathus, E., Pu, L.L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Parlmus, E., Pu, L.L., Quiles, M., Ren, Y., Roderyer, S., Scott, G., Shen, H., Shooshtari, N., Stone, H., Stone, H., Sodergren, B., Sonaike, T., Sparks, A., Tamerisa, K., Tang, H., Thomas, N., Thomas, S., Worley, K., Wu, Y. F., Zhou, J., Zorrilla, S., Watlington, S., Worley, K., Wu, Y. F., Zhou, J., Zorrilla, S., Watleng, D., Watling, G., Watlingson, S., Watleng, G., Watling, G., Watli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnGlyLysAspGlnHisPheProValPheMetAsnGluLysGluAspIleLeuTrpCys
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                                                         Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Weinstock, G. and Gibbs, R.
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                              Submission
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                                                                                           Zorrilla, S.,
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Baylor Plaza, Houston,
3 (bases 1 to 123936)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-JUL-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 12)
Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 123936)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of re
Assembly program: Phrap; version 0.990329
Consensus quality: 95907 bases at least Q40
Consensus quality: 99223 bases at least Q30
Consensus quality: 101036 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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Center clone name: CH230-282D16
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1101: contig of 2889 bp in length 31201: gap of unknown length 3415: gap of unknown length 34515: gap of unknown length 3753: contig of 2314 bp in length 3753: contig of 2314 bp in length 40938: contig of 2318 bp in length 40938: contig of 2318 bp in length 40938: contig of 3485 bp in length 41312: contig of 3293 bp in length 4431: gap of unknown length 55181: contig of 3046 bp in length 55181: gap of unknown length 65181: contig of 3046 bp in length 55181: gap of unknown length 65181: gap of unknown length 65181: gap of unknown length 65181: gap of unknown length 65182: contig of 4180 bp in length 65182: contig of 4180 bp in length 65182: gap of unknown length 67534: gap of unknown length 67535: contig of 5572 bp in length 67535: gap of unknown length 67535: gap 
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                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (B-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
                                                                                                                                                                                                                                           NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; CDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
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Shibahara, T., Tanaka, T.
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ArgPheLeuGluSerAsnProValMetIleAspAlaLysGluValSerAlaAlaHisArg
                                                                      PhePheTrpLeuPheGluAsnValValAlaMetGlyValSerAspLysArgAspIleSer
                                                                                                                                 PhePheGluPheTyrArgLeuLeuHisAspAlaArgProLysGluGlyAspAspArgPro
                                                                                                                                                                               AATGACCTCTCCATCGTCAACCCTGCTCGCAAGGGCCTCTACGAGGGCACTGGCCGGCTC
                                                                                                                                                                                                  AsnAspLeuSerIleValAsnProAlaArgLysGlyLeuTyrGluGlyThrGlyArgLeu
                                                                                                                                                                                                                                                                    ThrGlnLysHisIleGlnGluTrpGlyProPheAspLeuValIleGlyGlySerProCys
                                                                                                                                                                                                                                                                                                                                ThrValGlyMetValArgHisGlnGlyLySIleMetTyrValGlyAspValArgSerVal
                                                TTCTTCTGGCTCTTTGAGAATGTGGTGGCCATGGGCGTTAGTGACAAGAGGGACATCTCG
                                                                                                                 TTCTTTGAGTTCTACCGCCTCCTGCATGATGCGCGCCCAAGGAGGAGATGATCGCCCC
                                                                                                                                                                                                                                               ACACAGAAGCATATCCAGGAGTGGGGCCCATTCGATCTGGTGATTTGGGGGGCAGTCCCTGC
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471 IleAspGluArgThrArgGluArgLeuValTyrGluValArgGlnLysCysArgAsnIle
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                                                            LysAspLeuGlyIleGlnValAspArgTyrIleAlaSerGluValCysGluAspSerIle
                                                                                                                                                  AGGAAGCCCATCCGGGTGCTGTCTCTCTTTGATGGAATCGCTACAGGGCTCCTGGTGCTG
                                                                                                                                                                                                           ArgLysProIleArgValLeuSerLeuPheAspGlyIleAlaThrGlyLeuLeuValLeu
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AAGGACTTGGGCATTCAGGTGGACCGCTACATTGCCTCGGAGGTGTGTGAGGACTCCATC
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AF151974 4163 bp mRNA linear ROD 08-JUN-2000
Mus musculus DNA cytosine specific methyltransferase isoform 6
(Dnmtlb) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start*1
product="DNA cytosine-specific methyltransferase isoform
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Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
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Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Mu, G.Y. and
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                                   791 AlahrgTyrPheTrpGlyAsnieuProGlyMetAsnArgProLeuAlaSerThrValAsn 810
                                                                                                               811 AsplysleuGluLeuGlnGluCysLeuGluHisGlyArgIleAlaLysPheSerLysVal 830
                                                                                                                                                                                          831 ArgThrileThrThrArgSerAsnSerIleLysGlnGlyLysAspGlnHisPheProVal 850
                                                                                                                                                                                                                                                                    PheMetAsnGluLysGluAspIleLeuTrpCysThrGluMetGluArgValPheGlyPhe 870
                                                                                                                                                                                                                                                                                                                                               871 ProvalHisTyrThrAspValSerAsnMetSerArgLeuAlaArgGlnArgLeuLeuGly 890
902 CGATTTCTCGAGTCCAACCCTGTGATGATTGATGCCAAAGAAGTGTCAGGCTGCACACAGG 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Dnmt3b"
/function="methylates cytosine in DNA"
/note="alternatively spliced"
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/dev_stage="8-9 day old embryo"
1. .4163
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/db_xref="GI:8347131"
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297. .2816
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AF151974.1 GI:8347130
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/translation="MKGDSRHIABEEGASGYEECIIVNGNFSDQSSDTKDAPSPPVLE
TCTEPVCTPETRGRRSSSRLSKREVUSLLAYTQDWTGDGDRDDBVDGDGSDILMPK
LIRETKDTRTRSESPAVRTHSNGTSSLERQRASPRITRGRQGRHHYQEYPVEFPATR
SRRRRASSAAFPWSSPASYDPMEEVTPKSVGTPSVDLSQDGDQEMDTTQVDAESI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468 GGCCGCAGGTCAAGCTCCCGGCTGTCTAAGAGGGAGGTCTCCAGCCTTCTGAATTACACG 527
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ValGluGluAsnGlnGlyProGlyGlu 235 AGCACGCCATGGTCATCCCTGCCAGC 833 ValGlnGlnProThrAspProAlaSer 255 [
PyGlu 235 CAGC 833 aSer 255 -TCA 881 aThr 275 AGAG 941 AGAG 941 AGAG 112 Phet 315 CAAG 112 Phet 315 CAAG 112 Phet 315 CAAG 134 CA

RESU ACOO LOCU	B 6	4G 4G	d Ao	D 99	g 99	D &	D 07	B &	40 40	do Vo	D VQ	B 6	망양	B 64	dg VQ	40 VQ	B 64	Db
SULT 8 009474 CUS	89 275	269	263	834 2577	814 2517	79 245	239	233	734 2277	714 2217	215	2097	203	63 197	615 1917	595 1857	575 1797	(L)
AC009474	4 SerValProVallleArgHis	4 TyrThrAspValSerAsnMet:	4 GluLysGluAspIleLeuTrp(ThrThrArgSerAsnSerIle	GluLeuGlnGluCysLeuGl	4 PheTrpGlyAsnLeuProGlyMetAsnArgProLeuAlaSerThrV 	4 GluSerAsnProValMetileAspAl 7 GCATGTAACCCAGTGATGATCGATGC	4 LeuPheGluAsnValValAlaMetGlyValSerAspLysArgAs :::	4 PheTyrArgLeuLeuHisAspAla TrraccacTTGCTGAATTATACC	SerIleValAsnProAla	4 HislleGlnGluTrpGlyProl	MetValArgHisGlnGl	4 GlyIleGlnValAspArgTyrIleAl ::: :::: 7 GGTATTAAAGTGGAAAAGTACATTGC	4 IleArgValLeuSerLeuPhe 7 ATTAGAGTCCTGTCTCTGTTTC	GlnGluPheAspP ::: ::: CTGGAAGAATTTGAGC	LeuArgArgArgGluAspTr	AlaileLysGluAspPr	7 TGCAGATGCTTCTGTGTGGAGTGTCTGGAGGTGCTGGTGGGCGCAGGCACAGCTGAGGAT
168651 pp		SerArgLeuAlaArgG GGCCGCGGCGCCCGTC	euTrpCysThrGluMetGluA GTGGTGCACTGAGCTCGAAA	:LysGlnGlyLysAsp(::: :AGACAGGGCAAAAACC	uHisGlyArgIleAlaLy:	MetAsnArgProLeu <i>H</i> ATGAACAGGCCCGTG <i>H</i>	AspAlaLysGluValSerAlaAlaHi :::	MetGlyValSerAspi 	AlaArgProLysGluGlyAsp <i>P</i> ACCCGCCCAAGGAGGGCGAC <i>P</i>	ArgLysGlyLeuTyrGluGlyThrGlyArgLe CGCAAAGGTTTATATGAGGGCACAGGAAGGCT	roPheAspLeuVallleGlyGly GTTCGACTTGGTGATTGGTGGA	YLYSI1eMetTYrValGlYAs; -:: CCAGATCAAATATGTCAATGA	IleAlaSerGluValCy: ATTGCCTCCGAAGTCTGT	SerLeuPheAspGlyIleAlaThrGlyL TCTCTGTTTGATGGAATTGCAACGGGGT!	roProLysValTyrProProValPr ::: ACCCAAGTTGTACCCAGCAATTCC	pProSerArgLeuGlnMetP RAACATGCGCCTGCAAGACT	oTrpAsnCysTyrMetCysG ::: cTGGAGCTGCTATATGTGCC	TGTCTGGAGGTGCTGC
DNA	LysgluTy ::: ;AAGGACTA	lnArgieu ::: AGAAGCTG	ArgValPho ::: AGGATCTTO	pGlnHisPhel :: ACCAGCTTTTC	31. - 85	laserTh ::::: MGGCTTC	SerAlaAl CTGCTGC	ysargas ::: \agaaaga)lyAspAsp. ::: GCGACAAC	HyThrG1	HyGlyse	OVA CGT	YsGluAspSe ::: GTGCAGAGTC	HYLeuLeuVall	6 - S	101 101 101 101 101 101 101 101 101 101	GlyHisLyst	TGGGCGC
linear	/rPheAlaCy:	uLeuGlyArgS	eGlyPheP GGCTTCC	eProValPhe	heSerLysValAı : TAAAGAAAGTGC!	ırValAsnAspLy: : :AAAGAATGATAA	aHisArgAlaArg TCACAGGGCCCGC	SpIleSerArgPhe ACATCTCAAGATTC	pArgProPhePh : :CCGTCCATTCTT	YArgLeuPhei AAGGCTCTTC	ProCysAsnAs	ArgSerValTh ::: CCGGAAAATCAC	Prile	uValLeuLy: GGTGCTCAA	.aGluLysArgLy: :: AGCCAAAAGGAG	heAlaAsnAsnI - TCACTACTGAT	31yTh	'AGGCACAG
PRI 08-	ys 911 	rgSerTrp 3GTCCTGG	roValHis CTGCTCAC	neMetAsn CATGAAT	rgThrIle :: [:AGACAATA	spLysLeu \TAAGCTC	laArgTyr CCGGTAC	rgPheLeu GATTCCTG		hePheGlu CTTCGAG	snAspLeu rGATCTC	nrGlnLys ::: CCAAGAAA	ThrValGly GCTGTGGGA	ysAspLeu ::: AGGAGTTG	rgLysPro ::: GAGGCCC	snHisAsp :: aTCCTGAC	yrGlyLeu :: ::: ATGGGGTC	CTGAGGAT
-NOV-2000		893 2756	873 2696	853 2636	833 2576	813 2516	793 2456	773 2396	753 2336	733 2276	713 2216	693 2156	673 2096	653 2036	633 1976	614 1916	594 1856	1796

1. 166551 /organism="Homo sapiens" /db_xref="taxon:9606" /ch_omosome="2"

/clone="RP11-179G23" /clone_lib="RPCI-11" 13. .497 /rpt_family="L2"

"ap="2"

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The clone sequenced to the left is RP11-547F18; the clone sequenced to the right is RP11-444B4, 200 base pair overlap. Actual end of this clone is at base position 18711 of RP11-444B4.

Location/Qualifiers
                 VECTOR: PBACe3.6
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                                                                                                                 FEATURES
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Waterston, R.H.
Direct Submission
Submitted (124-AUG-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 168651)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                              Eukaryotari
Eukaryotari
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Malston, J. E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. B (11), 1097-1108 (1998)
Homo sapiens BAC clone RP11-179G23 from 2, complete sequence.
AC009474
                                                                                                                                                                                                                                                                                         (bases 1 to 168651)
Mulvane,E., Stoneking,T., LaPlant,Y. and McDill,B.
The sequence of Homo sapiens BAC clone RP11-179G23
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                                                                                                sapiens
                                                                                                                 Homo sapiens
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            DEFINITION
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VERSION
KEYWORDS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MC. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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MAPPING INFORMATION: restriction digest.

SOURCE INFORMATION:

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                       75913 AAAAAAGCTCGACATCAAGGAGATTGTTGATGAAC--ACAGAAGAGTAGTTAGTGTACAA
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                                                                    482 uValArgGlnLysCysArgAsnIleGluAspIleCysIleSerCysGlySerLeuAsnVa
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502 lThrLeuGluHisProLeuPheValGlyGlyMetCysGlnAsnCysLysAsnCysPheLe
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                                                    AGTGAGGAAGAAGTGCCAGAACATCAAGGACCTTTGTGTCTCTTGTGAGAGCCTCAATGT
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76031 CACTCTGGAACAGCCCCTCTTCATGCTAGGAATATGACGACATTGCAAGAACTGCTTCCT 76090
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                                                                                                                                                                                                                                                                                                                                                     76508 GTC-TCAGAGGTGTGTGAGGACGCCATCATTGTGGGCATGCTGTGGCACCAGGGGAGGAT 76566
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                                     522 uGluCysAlaTyrGlnTyrAspAspAspGlyTyrGlnSerTyrCysThrIleCysCysGl 542
                                                                                                           542 yGlyArgGluValLeuMetCysGlyAsnAsnAsnCysCysArgCysPheCysValGluCy 562
                                                                                                                                                                                 sValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLysGluAspProTrpAs 582
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AF068627 4135 bp mRNA linear ROD 06-DEC-1999 Mus musculus DNA cytosine-5 methyltransferase 3B2 (Dnmt3b) mRNA, alternatively spliced, complete cds.
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Direct Submitssion
Submitted (04-NOV-1999) CVRC, Mass. Gen. Hospital, 149 13th Street,
Charlestown, MA 02129, USA
Sequence update by submitter
Sequence update by submitter
On Nov 18, 1999 this sequence version replaced gi:3327981.
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GDSTEYQDDKEFGTGDLVWGTKGESWWPAMYVSWKATSKRGAMPGMRYWVQNFGDGKF
SELSADKLVALGLFSQHPKLATFWLLVSYRKAMYTLERCARVRAGKTFSSSPGESLED
QLKPMLEWAHGGFKPTGIEGLKPNKKQPENKSRRRTTUDSAASESPPPKRLKTNSYGG
KORGEDESRSERMASEVTWKGNLEDDKCLSGCKKVPVSFHPLFEGGLGGSCRDRFLEL
FYMYDEDGYGSYCTVCGRELLLCSNTSCCRCFCVECLEVLVGAGTAEDARLAGEW
CYMCLPQRCHGVLRRRKDWNMRLQDFFTTDPDLEEFEFPPKLYPAIPAAKRRPIRVLSL
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AICTEPVCTPETRGRRSSSRLSKREVSSLLNYTQDMTGDGDRDDEVDDCNGSDILMPK
LTRETKDTRTRSESPAVRTRHSNGTSSLERQRASPRITRGRQGRHHVQEYPVEFPATR
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Xie,S., Okano,M. and Li,E.
Direct Submission
Submitted (28-MAY-1998) CVRC, Mass. Gen. Hospital, 149 13th Street,
Charlestown, MA 02129, USA
3 (bases 1 to 4135)
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Cloning and characterization of a family of novel mammalian DNA (Cyroaine-5) methyltransferases

Nat. Genet. 19 (3), 219-220 (1998)
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/note="similar to EST sequences deposited in GenBank
Accession Numbers AA116694, AA119979, AA17277, AA210568,
AA407106, and AA575617
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/product="DNA cytosine-5 methyltransferase 3B2"
/protein_id="AAG40179.2"
/db xref="G1:6449472"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'function="de novo DNA methylation"
                                                                                                                             77198 CTTCCCTCCACTGAAGGGGTATTTTGCTTGTG 77231
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|db_xref="taxon:10090"
|chromosome="2"
                                                                                                       901 uPheAlaProLeuLysGluTyrPheAlaCysVal
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TyrTyrIleSerLysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGlu 215
                                          AGAATCACCCGAGGTCGGCAGGGCCGCCACCATGTGCAGGAGTACCCTGTGGAGTTTCCG
                                                                           ArgLeuThr----
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WGPFDLVIGGSPCNDLSNVNPARKGLYBGTGRLFFFEYHLLNYTTREKEGDNRFFFMMF
ENVVAMKVNDKKDISRFLACNPWIDAIKVSAAHRARYFMGNLFBWNRFVMASKNDKL
ELQDCLEFSRTAKLKXVQTITTKSNSIRQGKNQLFPVVMNGKDDVLWCTELERIFGFP
AHYTDVSNMGRGARQKLLGRSWSVPVIRHLFAPLKDYFACE"
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                                                                                                                                                                  ATTAGAGICCTGTCTCTGTTTGATGGAATTGCAACGGGGTACTTGGTGCTCAAGGAGTTG 2008
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                                               LeuArgArgArgGluAspTrpProSerArgLeuGlnMetPhePheAlaAsnAsnHisAsp 614
                                                                                                                                          634 IleArgValLeuSerLeuPheAspGlyIleAlaThrGlyLeuLeuValLeuLysAspLeu 653
                                                                                                                                                                                                                                       674 MetValArgHisGlnGlyLysIleMetTyrValGlyAspValArgSerValThrGlnLys 693
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Mus musculus DNA cytosine-specific methyltransferase isoform 2
(Dnmtlb) mRNA, complete cds.
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| Discretin_id:834712.0"
| translation="MKGDSRLSKREVSSLLNYTQDMTGDGDRDDEVDDGNGSDLMPK
| AICTEPVCTPETRGRRSSSRLSKREVSSLLNYTQDMTGDGDRDDEVDDGNGSDILMPK
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Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
P.R.China
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|product="DNA_cytosine-specific_methyltransferase_isoform
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and Shen, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cloning of full-length Dnmt3b cDNA and its alternative splicing isoforms in mouse embryonic tissue Upublished 2 (bases 1 to 4278)
Yin, B., Chen, Y. T., Zhu, M., Luo, Y. J., Zhu, N., Xu, S.C., Wu, G. Y. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ProAlaMetProSer---SerGlyProGlyAspThrSerSer-----AlaAlaGlu 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'function="methylates cytosine in DNA"
'note="alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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/dev_stage="8-9 day old embryo"
1. .4278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412. .2931
/gene="Dnmt3b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="Dnmt3b"
AF151970
AF151970.1 GI:8347119
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2225.00
59.24%
46.29%
45.09%
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                                                                                                                                       Mus musculus.
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Best Local Similarity:
Query Match:
DB:
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318 1184	<pre>yLysLeuArgGlyPheSerTrpTrpProGlyArgIleValSerTrpTrpMetThrGlyAr :::::: </pre>	298 1125	망양
298 1124	yAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeuValTrpGl	278 1065	ρ Q
1064		0 (B 3
i c	U	л н	5
258	SValGluGluAlaSerProProAlaValGlnGlnProThrAspProAlaSerProThrVa ::: ::: ::: ::: ::: CATGGAAGAAGTGACCCTTAAGAGCCTTCAGTTACCCCATAGTTGACTTT	238 957	B 8
956	GCATCGTCTTCAGCAAGCACGCCATGGTCATCCCCTGCCAGCGTCGACTT	907	рь
238	aLysValIleAlaGlyMetAsnAlaValGluGluAsnGlnGlyProGlyGluSerGlnLy	218	Ş
906		891	밁
ï	luTrpLeuAlaArgTrpLysArgGluAlaGluLysLy	198	Ş
198 890	rPheGlnAlaGlyAspProTyrTyrIl)189 831	B ox
830	AACCCGACATAGCAATGGGACCTCCAGCTTGGAGAGGCAAAGAGCCTCCCCCAGAATCAC	771	В
189	qLeuArgGlyGlyLeuGlYTrpGluSerSerLeuArgGlnArgProMetProArgLeuTh	169	Ş
7	CCAAA	\vdash	D
169	aGlyLysGluGlnLysGluThrAsnIleGluSerMetLysMetGluGlySerArqGlyAr	149	Ş
<u> </u>			d d
149	GluGlyArgGlyAlaProAlaGluAl	141	Qγ
650	GTCAAGCTCCCGGCTGTCTAAGAGGGAGGTCTCCAGCCTTCTGAATTACACGCAGGACAT	591	Дb
140		140	οy
590	- CCAGTCTTGGAGGCAATCTGCACAGAGCCAGTCTGCACACAGAGCCAGAGGCCGCAG	532	дb
140	roGluAlaSerArgAlaValGluAsnGlyCysCysThrPro	125	ş
531	ACCC	528	Дb
125	rProAlaGlyGlyGlnLysGlyGlyAlaProAlaGluGlyGluGlyAlaAlaGluThrLe	105	Ş
105 527	uLeuLeuProAsnGlyAspLeuGluLysArgSerGluProGlnProGluGluGlySe	468	B 3
467	AACAATGAAGGGAGACAGCAGACATCTGAATGAAGAAGAAGAGGGTGCCAGCGGGTATGAGGA	408	망
86	SerGlyAlas	81	Ş
	ដ	348	В
18	SerLysSerProSerMetAlaGlnAs	73	γQ
347		288	В
	oProValGluSerGlyAspThrProLysAspProAlaValIle	58	Ş
287	CCGCCGGCCAGGACCCGCGGCGCGCGATCGCGGCGCGCGC	228	Д
58	gGlnGluProSerThrThrAlaArgLysValGlyArgProGlyArgLysArgLysHisPr	38	8

676 gHisGlnGlyLysIleMetTyrValGlyAspValArgSerValT	ξ
21	Dβ
656 nValAspArgTyrileAlaSerGluValCysGluAspSerIleThrValGlyMet	Q
636 LeuSerLeuPheAspGlyIleAlaThrGlyLeuLeuValLeuLy&AspLeuGlyIleGL	B 6
616 uPheAspProProLysValTyrProProValProAlaGluLysArgLysProIleJ	8 8 8
597 gArgGluAspTrpProSerArgLe ::: 1980 CAGGAAAGATTGGAACATGCGCCT	B 8
577 sGluAspProTrpAsnCysTyrMetCysGlyHisLysGlyTl ::::: :: 1920 GCAGGAACCCTGGAGCTGCTATATGTGCCTCCCTCAGCGCTC	B 8
557 sPheCysValGluCysValAspLeuLeuValGlyPro	₽ &
537 sThrI1 :: 1800 CACCGT	음 성
517 sLysAsnCysPheLeuGluCysAlaTyx	라 성
497 sGlySerLeuAsnValThr	참 장
477 uArgLeuValTyrGluValAy ::: 1620 ACGGATGGCTTCTGAAGTCA	다 상
457 oArgLysSerThrAlaGluLysProLysValLysGluII	라
437 rAspMetTrpValGluProGluAlaAlaAlaTyrAlaPro :::::::	라 양
418 yProLysGlyLeuGluProProGluGluGluLysAsnProTyrLysGluValTy ::: ::: ::::::::::::::::::::	B 6
398 aValGluValGlnAsnLysProMetIleGluTrpAlaLe	₽ &
378 rArgAlaGlyLysLeuPheProValCysHisAspSerAspGluSerAspThrAla	라 상
358 rTyrAsnLysGlnProMetTyrArgLysAlaIleTyrGluValLeuGlnValA] ::: ::: 1305 CTTCAATAAGCTGGTTTCTTATAGGAAGGCCATGTACCACACTCTGGAGAAAGC	당양
338 IValCysValGluLysLeuMetProLeuSerSerPheCysSerAlai :::	B &
318 gSerArgAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAepGlyLyi ; ;;	Db Qy

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FHPLFEGGLCGSCRDRFLELFYMYDEDGYGSYCTVCCEGRELLLCGSTSCCRCFCVEC
ELVUCAGATAEDAKLQEPWSCYMCLPQFACGYULVKELGIKVEKYIAGDFFTPDFLEEFEP
PKLYPALPAKRRPITVLSLFDGTATGYLVLKELGIKVEKYIAGBVCAESIAVGTVKH
EGQIKYVNDVRKITKKNIEEWGPFDLVIGGSPCNDLSNVNPARKGLYEGTGRLFFFFY
HLLNYTRPREGDDRRPFWWFBNVYAKKVNDKXDISRFLAKOPWIDAIKVSAAHRARY
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MNGKDDVLWCTELERIFGFPAHYTDVSNMGRGARQKLLGRSWSVPVIRHLFAPLKDYF
                                                                                                                                                                                                                                                                                                                                                                                          SRRRAASSSASTPWSSPASVDPMEEVTPKSVGTPSVDLSQDGDQGGMDTTQVDBESTY
GDSTEYQDDKEFGIGDLVWGKIKGFGWWPAMYVSWKATSKRQAMPGMRWVQWFGDGKF
SEISADAKLVALGLFSQHFWLATFWKALVSYRKAMYTLEKARYARAGKTPSSSFGESLED
QLKBMLEMAHGGFFYTGIEGLKWKKQPVNKSKWRFSDSRULEPRRENKSRRTTN
DSAASESPPRKRKTNSYGGKDRGEDEESRERMASEVTNNKGNLEDBCLISCGKKQNPVS
                                                                                                                                                                                                                                                                                                                                   /translation="MKGDSRHLNEEEGASGYEECIIVNGNFSDQSSDTKDAPSPPV
AICTEPVCTPETRGRRSSSRLSKREVSSLLNYTQDMTGDGDRDDEVDDGNGSDILMPK
LTRETKDTRTRSESPAVRTRHSNGTSSLERQRASPRITRGRQGRHHVQEYPVEFPATR
                                                                                                                                                       297. .2876

// gene="Dnmt3b"

// function="methylates cytosine in DNA"

// note="allernatively spliced"

// codon start="

// product="DNA cytosine-specific methyltransferase isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 CCAAGTAAACGTAGCGCAGCGATCGGCGCCGGAGATTCGCGAACCCGAČÁCTCCGCGCG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 ------CCAGTCTTGGAGGCAATCTGCACAGAGCCAGTCTGCACACCAGAGACCAGA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           468 GGCCGCAGGTCAAGCTCCCGGCTGTCTAAGAGGGAGGTCTCCAGCCTTCTGAATTACACG 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 ProSerThrThrAlaArgLysValGlyArgProGlyArgLysArgLysHisProProVal 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 LysSerProSerMetAlaGlnAspSer-------GlyAlaSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 TATGAGGAGTGCATTATCGTTAATGGGAACTTCAGTGACCAGGCCCCAGACGAATGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 GluThrLeuProGluAlaSerArgAlaValGluAsnGlyCysCysThrProLys----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                            'db_xref="taxon:10090"
'dev_stage="8-9 day old embryo"
                                                                                                                                                                                                                                                                                             /protein_id="AAF74519.1"
/db_xref="GI:8347128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-720-086-7 (1-912) x AF151973 (1-4223)
  Location/Qualifiers
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                                                                                                                             /gene="Dnmt3b"
297. 2876
                                                         strain="KM"
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2223.50
59.81%
46.97%
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                   .4223
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Best Local Similarity:
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DB:
                     source
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FEATURES
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Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
P.R.China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus.
Buka musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 4223)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloning of full-length Dnmt3b cDNA and its alternative splicing isoforms in mouse embryonic tissue tombulishes to 4223)
Yin, B., Chen, Y.T., Zhu, M., Luo, Y.J., Zhu, N., Xu, S.C., Wu, G.Y. and
2220 GCATGAAGGCCAGATCAAATATGTCAATGACGTCCGGAAAATCACCAAGAAAATATTGA 2279
                                                                                  2280 AGAGTGGGGCCCGTTCGACTTGGTGATGGTGGAAGCCCATGCAATGATCTCTCTAACGT 2339
                                                                                                                                                                 2340 CAATCCTGCCCGCAAAGGTTTATATATGAGGGCACAGGAAGGCTCTTCTTCGAGTTTTACA 2399
                                                                                                                                                                                                                                         2460 GAATGTTGTGGCCATGAAAGTGAAAAAAAAAAAAACATCTCAAGATTCCTGGCATGTAA 2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2580 TAACCTACCCGGAATGAACAGGCCCGTGATGGCTTCAAAGAATGATGATAAGCTGGAGCTGCA 2639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2700 GTCGAACTCCATCAGACAGGCAAAAACCAGCTTTTCCCTGTAGTCATGAATGGCAAGGA 2759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2520 CCCAGTGATGATGGATGCCATCAAGGTGTCTGCTGCTCACAGGGCCCGGTACTTCTGGGG 2579
                                                                                                                                   716 1AsnProAlaArglysGlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrAr 736
                                                       696 nGluTrpGlyProPheAspLeuValileGlyGlySerProCysAsnAspLeuSerIleVa 716
                                                                                                                                                                                                                                                                                               uAsnValValAlaMetGlyValSerAspLysArgAspIleSerArgPheLeuGluSerAs 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                      796 yAsnLeuProGlyMetAsnArgProLeuAlaSerThrValAsnAspLysLeuGluLeuGl 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nGluCysLeuGluHisGlyArgIleAlaLysPheSerLysValArgThrIleThrThrAr 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gSerAsnSerIleLysGlnGlyLysAspGlnHisPheProValPheMetAsnGluLysGl 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uAspIleLeuTrpCysThrGluMetGluArgValPheGlyPheProValHisTyrThrAs 876
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                                                                                                                                                                                                                  736 gLeuLeuHisAspAlaArgProLysGluGlyAspAspArgProPhePheTrpLeuPheGl
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AF151973.1 GI:8347127
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DEFINITION
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AUTHORS
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JOURNAL
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700	WCWHCCWHI		t
ı Ü	alTyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProProProProAla	435	3 5
1460	GCGTCGTTCAGACAGTAGGAACTTAGAACCCAGGAGACGCGAGAACAAAAGTCGAAGA	1401	뮹
434	ProGluGluGluLysAsnProTyrLysGlu	425	á
1400	aagcaaccagtggttaataagtcgaag	1341	뮹
424	roSerGlyProLysGlyLeuGluPro	416	ξ
1340	CCACGGTGGCTTCAAG	1281	岁
415	laValGluValGlnAsnLysbroMetIleGluTrpAlaLeuGlyGlyPheGln	396	ξ
N	TCCAGCAGTCCT	424	귱 :
395	erArgAlaGlyLysLeuPheProValCysHisAspSerAspGluSerAspThr	376	ξ
1241	GIDALA INTIYEASDLYBGIDETOMOCIYEATGLYBALGEIYEGIUVALLEUGIDVAI ::: ::: 	1182	8 8
ıi	3	1	
355 1181	PheSerValValCysValGluLysLeuMetProLeuSerSerPheCysSerAlaPheHis 	336	ყჳ
1121	TGGTTTGGTGATGGCAAG	1062	岁
335	rGlyArgSerArgAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLys	316	ξ
0	AAGCC	0	岁
315	alTrpGlyLysLeuArgGlyPheSerTrpTrpProGlyArgIleValSerTrpTrpMet	296	¥
1001	CATATATGGAGACAGCACAGAGTATCAGGATGATAAAGAGTTTGGAATAGGTGACCTC	942	岁
295	spGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeu	276	¥
941	TGACTTGAGCCAGGATGGAGATCAGGAGGGTATGGATACCACACAGGTGGATGCAGAG	882	8
275	hrValAlaThrThrProGluProValGlySerAspAlaGlyAspLysAsnAlaThr	256	Ą
881	TIGGAAGAAGTGACCTAAGAGCGTCAGTACCCCATCA	834	岁
255	lnLysValGluGluAlaSerProProAlaValGlnGlnProThrAspProAlaSer	236	Ϋ́
833		792	ğ
235	AlaLysValIleAlaGlyMetAsnAlaValGluGluAsnGlnGlyProGlyGlu	216	₹
791	TCGGAGACGTCGA	768	8
215	LysArgLysArgAspGluTrpLeuAlaArgTrpLysArgGluAlaGlu	961	ž
767	AATCACCCGAGGTCGGCAGGGCCGCCACCATGTGCAGGAGTACCCTGTGGAGTTTCCG	708	$\frac{1}{2}$
195	PheGlnAlaGlyAspPro	187	₹
707	GCAATGGGACCTCCAGCTTGGAGAGGCAAAGAGCCTCCCCC	648	퓻
186	GlyArgLeuArgGlyGlyLeuGlyTrpGluSerSerLeuArgGlnArgProMetPro	167	¥
647	::: ACACCAGGACGCGCTCTGAAAGCCCG	588	ğ
166	luThrAsnIleGluSerMetLysMetGluGlySer	147	×
8	GGACATGACAGGAGATGAGACAGAGATGATGAGGTAGATGATGGGAATGGCTCTGAT	528	Ř
146	GluGlyArgGlyAlaPro	141	₹

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ROD 06-DEC-1999
(Dnmt3b) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xie,S., Okano,M. and Li.L.
Direct Submission
Submitted (28-MAY-1998) CVRC, Mass. Gen. Hospital, 149 13th Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (04-NOV-1999) CVRC, Mass. Gen. Hospital, 149 13th Street, Charlestown, MA 02129, USA Sequence update by submitter on Nov 18, 1999 this sequence version replaced gi:3327979.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 4155)

Okano, M., Xie, S. and Li, E.

Cloning and characterization of a family of novel mammalian DNA

(Cytosine-5) methyltransferases

Nac. Genet. 19 (3), 219-220 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to EST sequences deposited in GenBank
Accession Numbers AA116694, AA119979, AA17277, AA210568,
AA407106, and AA575617"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="de novo DNA methylation"
/fore="alternatively spliced product; contains Cys-rich
region; C-terminal region is similar to corresponding
region of DNA cytosine-5 methyltransferase 3A"
                                                                                   2637 ACCACCAAGTCGAACTCCATCAGACACGCGAAAAACCAGCTTTCCCTGTAGTCATGAAT 2696
                                                                                                                                                                     2697 GCCAAGGACGATTTGTGGTGCACTGAGCTCGAAAGGATCTTCGGCTTCCCTGCTCAC 2756
2757 TACACGGACGTGTCCAACATGGGCCGCGCGCCCCTCAGAAGCTGCTGGGCAGGTCCTGG 2816
                                                                                                                                        854 GluLysGluAspIleLeuTrpCysThrGluMetGluArgValPheGlyPheProValHis 873
                                                             834 ThrThrArgSerAsnSerlleLysGlnGlyLysAspGlnHisPheProValPheMetAsn 853
                                                                                                                                                                                                                            TyrThrAspValSerAsnMetSerArgLeuAlaArgGlnArgLeuLeuGlyArgSerTrp 893
                                                                                                                                                                                                                                                                                                      /product="DNA cytosine-5 methyltransferase 3B1"
/protein_id="AAC40178.2"
/db_xref="G1:6449470"
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chromosome="2"
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,S., Okano,M. and Li,E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 GCGGCCCAAGTAAACGTAGCGCAGCGATCGGCGCGCGGAGATTCGCGAACCC----GAC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 CCTCACGACAGGCCCGCTGAGGCTTGTGCCAGAACCTTGGAAACCTCAGGTATATACCTTT
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514	<pre>IleSerCysGlySerLeuAsnValThrLeuGluHisProLeuPheValGlyGlyMetCys 5</pre>	495	Ş
1588	AGCCGAGAACGGATGGCTTCTGAAGTCACCAACAACAAGGGCAATCTGGAAGACCGCTGT 1	1529	뮍
194	ArgGluArgLeuValTyrGluValArgGlnLysCysArgAsnIleGluAspIlo	475	8
1528	 ::: CGGGAAGGACCGAGGGGAG	1478	ర్జ
174	GluIleIl	455	5
154 L477	ValTyrThrAspMetTrpValGluProGluAlaAlaAlaTyrAlaProProProProAla 4 :::	435 1433	음 성
	 	1373	망
134	ProGluGluGluLysAsnProTyrLysGlu 4	425	5
1372	CTACTGGGATCGAGGGCCTCAAACCCAACAAGAAGCAACCAGTGGTTAATAAGTCGAAG	1313	B
124		416	Ş
115 1312	AlaLysAlaValGluValGlnAsnLysProMetIleGluTrpAlaLeuGlyGlyPheGln 4 :::::::::	396 1253	B 8
195	AlaSerSerArgAlaGlyLysLeuPheProValCysHisAspSerAspGluSerAspThr 3	376 214	B S
175	ATAC	1154	용 성
, ju	TIGAGATCTCTGCTGACAAACTGGTGGCTCTGGGGCTTTCAGCCAGC	ەت ر	용
155	PheSerValValCysValGluLysLeuMetProLeuSerSerPheCysSerAlaPheHis 3	336	Ş
135	ThrGlyArgSerArgAlaAlaGluGlyThrArgTrpValMetTrpPheGlyAspGlyLys 3	316 1034	음 성
1033	VALTIPGLYLYSLENAIGGLYPHESETTPTTPPROGLYARGILEVALSETTPTTPMET 3	296 974	용 성
- 7	Ω·	-	용
195	LysAlaGlyAspAspGluProGluTyrGluAspGlyArgGlyPheGlyIleGlyGluLeu 2	276	δ
113	FIGURE VALALATHETHEFOGUEFOVAL CLYSETABPATAGLYASPLYBASHALATHE Z STIGACTIGAGCCAGGATGGAGATCAGGAGGGTATGGATACCACACAGGTGGATGCAGAG 9	854	8 8
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OLKPRILBYAHGGRRETGIEGLKBVKKOPVNKSKYRKRSDSRULEPRRERBKSRRTTYD
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PHPLFEGGLCQSCRDRFLELFYMYDEDGYQSYCTVCCEGRELLLCSNTSCCRCFCVEC
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EGQIKYVNDVRKITKKNIEBWGPFDLVIGGSPCNDLSNVNPARKGLYBGTGRLFFFFY
HILNYTRPREGDRIRPFWMFRNYVAMKNTNDKLIEJSRFLACHWYDNIDAIRGSAGTGRLFFFFY
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MNGKDDVLWCTELERIFGPPAHYTDVSNMGRGARQKLLGRSWSVPVIRHLFAPLKDYF
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SRRRASSASTPWSSPASVDFMEEVTPKSYSTPSVDLSQDGDQEGNDTTQVDABSIY
GDSTEYQDDKEFGIGDLWGKIKGFSWWPAMVUSWKATSKRQAMPGMRWVWFFGDGKF
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Submitted (17-MAY-1999) Department of Biochemistry and Molecular
Biology, Institution of Basic Medical Sciences, Chinese Academy of
Medical Sciences, Dong Dan San Tiao 5, Beijing City 100005,
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/product="DNA cytosine-specific methyltransferase isoform
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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fin,B., Chen,Y.T., Zhu,M., Luo,Y.J., Zhu,N., Xu,S.C., Wu,G.Y. and
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                                                              2729 TACACGGACGTGTCCAACATGGGCCGCGCGCCCCTCAGAAGCTGCTGGGCAGGTCCTGG 2788
2669 GGCAAGGACGATTTTGTGGTGCACTGAGCTCGAAAGGATCTTCGGCTTCCCTGCTCAC 2728
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                                   874 TyrThrapValSerAsnMetSerArgLeuAlaArgGlnArgLeuLeuGlyArgSerTrp 893
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Mus musculus DNA cytosine-specific methyltransferase isoform 1
(Dnut2b) mRNA, complete cds.
                                                                                                                /gene="Dnmt3b"
/function="methylates cytosine in DNA"
/note="alternatively spliced"
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                                                  sPheCysValGluCysValAspLeuLeuValGlyProGlyAlaAlaGlnAlaAlaIleLy 577
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/protein id="AAL57040.1"
/db_xref="GI:18031252"
/translation="WKGDTRHLNGEEDAGGREDSILVNGACSDQSSDSPPILEAIRTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIRGRRSSSRLSKREVSSLLSYTODLTGDGDGEDGDGSDTPWAPKLFRETRTRSESPA
VRTRININSVSSRERHRPSPRSTRGRQGRIHVDESPVEFPATRSLRRRATASAGTPWPS
                                                                                               Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria, Primates; Catarrhini, Hominidae; Homo. I, Chases I to 4335)
Ni, J., Pradhan, S. and Roberts, R.J.
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                                                                                                                                                            Ni,J., Pradhan,S. and Roberts,R.J.
Cloning, expression and characterization of human DNMT3 genes
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                                                                                                                                                                                                                                                2 (bases 1 to 4335)
Ni,J., Pradhan,S. and Roberts,R.J.
Direct Submission
Submitted (122-DEC-2000) New England Biolabs, 32 Tozer Road,
Beverly, MA 01915, USA
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/db_xref="taxon:9606"
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/gene="DNMT3B"
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1 (bases 1 to 4267)

Xu,G.-L., Bestor,T.H., Bourc'his,D., Hsieh,C.-L., Tommerup,N., Bugge,M., Hulten,M., Qu,X., Russo,J.J. and Viegas-Pequignot,E. Chromosome instability and immunodeficiency syndrome caused by mutations in a DNA methyltransferase gene

Nature (1999) In press

2 (bases 1 to 4267)
                                                                                                                             Submitted (06-AUG-1999) Genetics and Development, University, 701 West 168 St., New York, NY 10032, Location/Qualifiers 1. 4267
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/note="mutated in human chromosome instability and immundeficiency disease known as ICF syndrome; contains alternative 5, exon 1B"
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901 2766	y 882 ArgLeuAlaArgGlnArgLeuLeuGlyArgSerTrpSerValProValIleArgHisLeu 	음 성
881 2706	y 862 ThrGluMetGluArgValPheGlyPheProValHisTyrThrAspValSerAsnMetSer	유 성
861 2646	842 GlnGlyLysAspGlnHisPheProValPheMel	음 5
841 2586	822 GlyArgIleAlaLysPheSerLysValArgThrI 2527 AATAGGATAGCCAAGTTAAAGAAAGTACAGACAA	유 성
821 2526	802 AsnArgProLeuAlaSerThrValAsnAs; :: ::::: AACAGGCCCGTGATAGCATCAAAGAATGA	유 성
801 2466	782 AlaLyBGluValSerAla ::: 2407 GCCATCAAAGTTTCTGCT	유 성
781 2406	762 GlyValSer/	F 9
761 2346	y 742 ArgProLysGluGlyAspAspArgProPhePheTrpLeuPheGluAsnValValAlaMet	B
741 2286	722 GlyLeuTyrGluGlyThrGlyArgLeuPhePheGluPheTyrArgLe	B 원
721 2226	702 AspLeuVallleGlyGlySerProCysAsnAspLeuSerIleValAsnProAlaAr	B 8
701 2166	682 MetTyrValGlyAspValArgSerValThrGlnLysHi	B 5
681 2106	662 AlaSerGluValCysGluAspSerIl	음 성
	642 GlyIleAlaThrGlyLeuLeuValLeuLysAspLeuGlyIleGlnValAspArgTyr	유 성
641 1986	\$22 ValTyrProProValProAlaGluLysArgLy(::: 1927 CTGTACCCTGCCATTCCCGCAGCCCGAAGGCG	B 8
621 1926	602 ProSerArgLeuGlnMetPhePheAlaAsnAsnHis7	음 성
601 1866	582 AsnCysTyrMetCysGlyHisLysGlyThrTyrGlyLev ::: : 1807 AGCTGTTACATGTGTCTCCCGCAGCGCTGTCATGGCGTV	유 성
581 1806	562 CysValAspLeuLeuValGlyProGlyAlaAlaGlnAla	B
561 1746	542 GlyGlyArgGluValLeuMetCysGlyAsnAsnAsnCy	무양

Search completed: November 22, 2002, 10:57:33 Job time: 5471.49 secs

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Sequence 35, Appl
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Sequence 46, Appl
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ALIGNMENTS

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RESULT 1
US-09-276-531-47
; Sequence 47, Application US/09276531
; Patent No. 6183968
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Reddy, Roopa
APPLICANT: Reddy, Roopa
APPLICANT: Reddy, Roopa
APPLICANT: Baughn, Mariah R.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
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TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC COMPATIBLE
COUNTRY: USA
ZIP: 94304
COMPUTER: LBM PC COMPATIBLE
COMPUTER: LBM PC COMPATIBLE
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                                ACCAAAACCACAGTGCCGACAGCTCTCCAATACTCAGGTTAATGCTGAAAAAATCATCCAA 1017
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TCGTTTTTTCCCAGGGCAAGCAGAAG----AGAAAATGTTGTATATGTGT----TTTTACC 1176 TOGCACCTTCCCCTTGCTTTCGTACAAGGCTGAAAGGCTGAAAGGCCTGATGG- ----TCTTGTAG- 1936 CATTTCCCAGGATGATGATGTCAGCAGGGATGACATCACCACC 3516

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Part No. 6183968
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION USATA:
APPLICATION USATA:
APPLICATION HEREWITH
CLASSIFICATION:
CLASSIFICATION
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                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: March 2:
CLASSIFICATION:
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APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF LIVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION:—RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
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ADDRESSEE: INCYTE PHARMACEUTICALS,
ATTORNEY/AGENT INFORMATION
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COLUMN TO THE PHARMAC CITY: 9ALO ALTO STATE: CALTO COTTON
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                                                 UMBER: 60/079,677
March 27, 1998
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INFORMATION FOR SEQ ID NO:
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IMMEDIATE SOURCE:
TERRARY: TESTTUT02
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REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA.
TELECOMMUNICATION INFORMATION:
TELECPHONE: (650) 855-0555
                          903 GluTyrPheAlaCys 907
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TYPE: nucleic acid
STRANDEDNESS: single
   GACTACTTTGCATGT
                                                              AAGCTGCTGGGAAGGTCCTGGAGCGTGCCTGTCATCCGACACCTCTTCGCCCCCTCTGAAG
                                                                                     ArgLeuLeuGlyArgSerTrpSerValProVall1leArgHisLeuPheAlaProLeuLys
                                                                                                                                       NTCTTTGGCTTTCCTGTGCACTACACAGACGTGTCCAACATGGGCCGTGGTGCCCGCCAG
                                                                                                                                                               ValPheGlyPheProValHisTyrThrAspValSerAsnMetSerArgLeuAlaArgGln
                                                                                                                                                                                                                 CTTTTCCCTGTTGTCATGAATGGCAAAGAAGATGTTTNGTGGTGCACTGAGCTCGAAAGG
                                                                                                                                                                                                                                        HisPheProValPheMetAsnGluLysGluAspIleLeuTrpCysThrGluMetGluArg
                                                                                                                                                                                                                                                                                                                                                                                       SerThrValAsnAspLysLeuGluLeuGlnGluCysLeuGluHisGlyArgIleAlaLys 822
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					transferase		astic disorder;	DNMT3A.					ii Ciicimi Cuit y	Human prostate exp	prostate ex	immume	Tumon immune syste	angiogene	Ξ.	n prostate			Human ovarian canc Human ovarian canc	Human genome-deriv		Probe #2439 for ge Probe #2546 used t	P# P		_ ~		- 100	DNA encoding novel		Gene #3887 used to	ne signat	DNA encoding novel

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methyltransferase designated DNAT3A. The polypeptides can be administered

therapeurically, especially by expressing encoding polynucleotides, to

treat diseases associated with DNA cytosine methyltransferase, such as

conclusion diseases associated with DNA cytosine methyltransferase, such as

conclusion of dispose, or determine susceptibility to neoplastic disorders,

be used to diagnose, or determine susceptibility to neoplastic disorders,

conclusion they are useful to screen for compounds inhibiting activating the

conclusion of DNA. Such in vitro methylation may be used to anyour

crequiate DNA expression in biological systems, e.g. recombinant DNA

conclusion to vitro may be introduced into a cell/organism to increase

conclusion to vitro may be introduced into a cell/organism to increase

conclusion to vitro methylated. The polypeptides can also be

used to produce antibodies which are useful to detect and purify the

colypeptide or therapeutically e.g. to treat neoplastic disorders. The

polyputoleotides are useful to produce probes and primers which are

cuseful diagnostically.
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99.8%; Score 4283.4; DB 21; Length 4416;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4287; Conservative 0; Mismatches 6; Indels 0; G
                                                                                                                                                                New mouse and human polypeptides, useful to treat and diagnose neoplastic disorders e.g. carcinomas, sarcomas and leukemias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4416 BP; 1107 A; 1131 C; 1327 G; 851 T; 0 other;
                                                                                                                                                                                                                                                                    Claim 10; Fig 1C; 114pp; English
   Okano M, Xie S;
                                                                   WPI; 2000-106298/09.
P-PSDB; AAYS4057.
   Li E,
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qq	664	GAGCCCTGCTGGGGGGGGGAGAAGGGCGGGGGCCCCAGCAGAGGGAGAGGGGGG
δ	601	
q	724	CCTGCCTGAAGCCTCAAGAGCAGTGGAAAATGGCTGCTGCACCCCCAAGGAGGGCCGAGG 783
ò	661	661 AGCCCCTGCAGAAGCGGGCAAAGAACAGAAGCAGCAACCAAC
đ	784	AGCCCCTGCAGAAGCGGGCAAAGAACAGAAGGAGACCAACATCGAATCCATGAAAATGGA 843
ò	721	GGGCTCCCGGGCCGGCTGCGGGGTGGCTTGGGCTGGGAGTCCAGCCTCCGTCGGCGGCC 780
අ	844	GGGCTCCCGGGGCCGGCTGCGGGGGGCTTGGGCTGGGAGTCCAGCCTCCGTCAGCGGCC 903
ò	781	CATGCCGAGGCTCACCTTCCAGGCGGGGACCCCTACTACATCAGCAAGCGCAAGCGGGA 840
g	904	carácceaascreacerrecaseceses de aceses de aceses de aceses de seguina esta esta esta esta esta esta esta est
ò	841	CGAGTGGCTGGCACGCTGGAAAAGGGAGGCTGAGAAAAAAAA
qq	964	cdagtegettégeacéctegaaaaggaaggetgagaaaaagecaaggteattécagaaat 1023
ð	901	GAATGCTGTGGAAGAAACCAGGGGCCCGGGAGTCTCAGAAGGTGGAGAGGAGGGCCAGCC 960
d G	1024	GAATGCTGTGGAAGAAAACCAGGGGCCCGGGGAGTCTCACAAGGTGGAGGAGGCAGCCA 1083
ò	196	TCCTGCTGTGCAGCAGCCCACTGACCCCGCATCCCCCACTGTGGCTACCACGCCTGAGCC 1020
qq	1084	recretaristaces de contrate de
ò	1021	CGTGGGGTCCGATGCTGGGGACAAGAATGCCACCAAAGCGGGGGATGACGAGCCAGAGTA 1080
QC C	1144	CGTGGGGTCCGATGCTGGGGACAAGATGCCACCAAAGCAGGCGATGACGAGCCAGAGTA 1203
ò	1081	CGAGGACGGAGGCTTTGGCATTGGGAACTGGTGTGGGGGAAACTGCGGGGCTTCTC 1140
q	1204	CGAGGACGGCCGGGGCTTTGGCGATTGGGGAGCTGGTGGGGGGAAACTGCGGGGCTTCTC 1263
ò	1141	CTGGTGCCCAGGCCGCATTGTGTTGGTGATGACGGCCCGGAGCCGAGCTGAAGG 1200
g G	1264	CTGGTGGCCAGGCCGCATTGTGTTTGGTGGATGACGGGCCGGAGCCGAGCAGCTGAAGG 1323
ò	1201	CACCCGCTGGGTCATGTGGTTCGGAGACGGCAAATTCTCAGTGGTGTGTTGAGAAGCT 1260
đ	1324	CACCCGCTGGGTCATGTGGTTCGGAGACGGCAAATTCTCAGTGGTGTGTGT
ò	1261	GATGCCGCTGAGCTCGTTTTGCAGTGCGTTCCACCAGGCCACGTACAACAAGCAGCCCAT 1320
q	1384	GATGCCGCTGAGCTCGTTTTGCAGTGCGTTCCACCAGGCCCACGTACAACAAGCAGCCCAT 1443
δ	1321	GTACCGCAAAGCCATCTACGAGGTCCTGCAGGTGGCCAGCGGCGGCGGGGAAGCTGTT 1380
Q	1444	GTACCGCAAAGCCATCTACGAGGTCCTGCAGGTGCCAGCAGCCGCGGGGGAGAGCTGTT 1503
ò	1381	CCCGGTGTGCCACGACAGCGATGAGAGACACTGCCAAGGCCGTGGAGGTGCAGAAA 1440
qq	1504	CCCGGTGTGCCACGACGGATGAGAGTGACACTGCCAAGGCCGTGGAGGTGCAGAACAA 1563
ò	1441	GCCCATGATTGAATGGGCCCTGGGGGCTTCCAGCCTTCTGGCCCTAAGGGCCTGGAGCC 1500
qq	1564	GCCCATGATTGAATGGGCCCTGGGGGCTTCCAGCATTATGGCCCTAAGGGCCTGGAGCC 1623
δ	1501	ACCAGAAGAAGAAGAATCCCTACAAAGAAGTGTACACGGACATGTGGGTGG
đ	1624	ACCAGAAGAAGAAGAATCCCTACAAAGAAGTGTACACGGACATGTGGGTGG
ò	1561	GGCAGCTGCCTACGCACCTCCACCAGCCAAAAGCCCCGGAAGAGACACAGCGGAGAA 1620
q	1684	GOCAGCTGCATACGCACCACCTCCACCAGAAAAGCCCCGGAAGAGCACAGCGGAGAA 1743
ò	1621	621 GCCCAAGGTCAAGGAGATTATTGATGAGCGCACAAGAGGCGGCTGGTGTACGAGGTGCG 1680
đ	1744	GCCCAAGGTCAAGGAGTTATTGATGAGGGCACAAGAGAGCGGCTGGTGCGAGGTGCG 1803

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Qy	B 8	B 8	B 8	B 8	B 8	B 8	B 64	B 8	B 8	B &	B 8	B 8	B 8	B 8	B 8	B 8	B 8	D
3841 TTCAAACAGCGAGATGAGTAAAAACATCAGCTTCCACGTTGCCTTCTGCGCAAAGGGTTT 3900	3781 TGAGATATATATATAAAGGTACTGTTAACTACTGTACAACCCGACTTCATAATGGTGCT 3840 	3721 AATCAGTTTCTAGAAGCCGCTGTTACCTCTTGTTTACAGTTTATATATA	3661 CCACACAAGACATTTTTCTACAGTATTTCAGGTGCCTACCACACAGGAAACCTTGAAGAA 3720 	3601 GCCAGCACCATTCCTGGTCACGCAAAACAGAACCCAGTTAGCAGCAGGAGAGGAGACGAGAACA 3660 	3541 GGGACGGAAAGAGAGAGACACTCAGGCGGCAGCATTCCCTCCC	3481 TITITIACTATATATCTTTTTTTTTTGTCTCTAGCCTGATCAGATAGGAGCACAAGCAG 3540 	3421 GAAATCTATATATIGGGTIGTITITTTTITIGTTTTTTIGGTTTTTTTT	3361 ATAGTAACAATACCTTGCAGAGGAAAGGTGGGAGGAGAGAAAAAAAGGGGAAATTTTTAAA 3420 	3301 TTTTGTTTCTTGCTGTGACTGAAACAAGAAGGTTATTGCAGCAAAAATCAGTAACAAAAA 3360 	3241 TITITICGGTCAGACCTITITATTITCTACTCTTTTCAGAGGGGTTTTCTGTTTGTTTGGG 3300 	3181 TATTCTTCAGTCCTATTTAAAAACAAAACCAAGCTCCCTTCCCTTCCCTTCCCCTTCCCTT 3240	3121 AATACCGGAGGGCTTTGCCTTGCGAAAAGGGTTGGACATCATCTCCTGATTTTTCAATGT 3180 	3061 AGAGAAGTATCAGCACCCAGAAGAGAAAAAAGGAATTTAAAACAAAAACCACAGAGGCGGA 3120 	3001 AAGTTAAACAAACAAACAAAAAAACACAAAACATAATAAAACACCAAGAACATGAGGATGG 3060 	2941 GCTGAAGGAGTATTTTGCGTGTGTGTAAGGGACATGGGGGCAAACTGAGGTAGCGACACA 3000 	2881 GAGGCAGAGACTGCTGGGCCGGTCATGGAGCGTGCCAGTCATCCGCCACCTCTTCGCTCC 2940	2821 GGANAGGGTATTTGGTTTCCCAGTCCACTATACTGACGTCTCCAACATGAGCCGCTTGGC 2880 	2761 AGACCAGCATTTTCCTGTCTTCATGAATGAGAAAGAGGACATCTTATGGTGCACTGAAAT 2820

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                                                                                                                                                                                                                                                                                                    CAGAACTAATCCAGAGTGTGGGAAAGTGACAGTCAAAACCCCCACCTGGAGCAAATAAAAA 4260
                                                                                                                                                                                                                                                                                                                    4264 ACGGAGTCTTCAGGCCCAGTTTCTCACTTTAGCCAATTCGAGGGCTCCTTGTGGTGGT 4323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                De novo DNA cytosine methyltransferase; Dnmt3a; neoplastic disorder; carcinoma; sarcoma; leukaemia; DNA methylation; ss.
3964 TTCAAACAGCGAGATGAGTAAAAACATCAGCTTCCACGTTGCCTTCTGCGCAAAGGGTTT
                                        CACCAAGGATGGAGAAAGGGAGACAGCTTGCAGATGGCGCGTTCTCACGGTGGGCTCTTC
                                                         4024 CACCAAGGATGGAGAAAGGAGAACAGCTTGCAGATGCCGCGTTCTCACGGTGGCTTTTC
                                                                                                          4084 CCCTTGGTTTGTAACGAAGTGAAGGAGAGAACTTGGGAGCCAGGTTCTCCCCTGCCAAAA
                                                                                                                                                                     4144 AĞĞĞĞĞÇTAĞATGAĞĞTĞĞTÇĞĞÇÇĞTĞĞAÇAĞCTĞAĞAĞTĞĞĞATTCATÇÇAĞACTÇ
                                                                                                                                                                                                              4204 ATGCAATAACCCTTTGATTGTTTTCTAAAAGGAGACTCCCTCGGCAAGATGGCAGAGGT
                                                                                                                                                                                                                                                 4141 ACGGAGTCTTCAGGCCCAGTTTCTCACTTTAGCCAATTCGAGGCCTCCTTGTGGTGGGAT
                                                                                           CCCTTGGTTTGTAACGAAGTGAAGGAGAGAACTTGGGAGACCAGGTTCTCCCTGCCAAAA
                                                                                                                                           AGGGGGCTAGATGAGGTGGTCGGGCCCCGTGGACAGCTGAGAGTGGGATTCATCCAGACTC
                                                                                                                                                                                               ATGCAATAACCCTTTGATTGTTTTCTAAAAGGAGACTCCCTCGGCAAGATGGCAGAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "de novo DNA cytosine methyltransferase Dnmt3a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mouse and human polypeptides, useful to treat and diagnose neoplastic disorders e.g. carcinomas, sarcomas and leukemias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding de novo DNA cytosine methyltransferase Dnmt3a.
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217..2943
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ37095 standard; DNA; 4192
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P-PSDB; AAY54055.
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The present sequence encodes a murine de novo DNA cytosine methyltransferase designated Dnmt3a. The polypeptides can be administered methyltransferase designated Dnmt3a. The polypeptides can be administered therapetrically wespecially by expressing encoding polynucleorides, to treat diseases associated with DNA cytosine methyltransferase, such as neoplastic disorders e.g. carcinomas, sarcomas and leukemias. They can be used to diagnose, or determine susceptibility to neoplastic disorders, by assaying for polypeptide expression levels in mammalian cells/body fluids. They are useful to screen for compounds inhibiting/activating the polypeptide expression levelylation may be used to direct or regulate DNA expression in biological systems, e.g. recombinant DNA methylated in vitro may be introduced into a cell/organism to increase or decrease expression of a desired polypeptide for which the native DNA is under-methylated or not methylated. The polypeptides can also be used to produce antibodies which are useful to detect and purify the polypeptide are useful to produce probes and primers which are useful diagnostically.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 GACAGAGGACCGTTCACCAGAGGGCTCAACACGGGATCTATGTTTAAGTTTTAACTCT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 66.9%; Score 2870.2; DB 21; Length 4192; Best Local Similarity 83.7%; Pred. No. 0; Matches 3573; Conservative 0; Mismatches 584; Indels 113; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 CCGGGCCGCCCGACCCGCGGCCACAGGCAGAGCCCCCTGAAGCCCCAGCGCTGAGGCT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 TGCTTACAAAGACCACGGCAATTCCTTCTGAAGCCCTCGCAGCCCCACAGGGGCCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACCACCACAGTCTCAGCCCATGGCCCAGGACTCTGGCCCCTCAGATCTGCTACCCAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 CGCCTCCAAAGACCACGATAATTCCTTCCCCAAAGCCC-AGCAGCCCCCCAGG-CCCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 TGGCCGGAAGCGCAAGCACCCACCGGTGGAAAGCAGTGACACCCCCCAAGGACCCAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 502 GGACTTGGAGAAGCGGAGTGAGCCCCAGCCAAGAGGAGGAGCCCTGCTGGGGGGGCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       540 GGGTGGGGCCCCAGCTGAAGGAGAGGG---AACTGAGACCCCACCAGAAGCCTCCAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               622 AGTGGAAAATGGCTGCTGCACCCCCAAGGAGGGCCCGAGGAGCCCCTGCAGAAGCGGGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     597 rgrágagaatigáctigergreaccaaddaagaccergágageererfacagaagagagaaa
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4192 BP; 1095 A; 1070 C; 1182 G; 844 T; 1 other;
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2782 CATGAATGAGAAAGGACATCTTATGGTCCACTGAAATGGA	4d 40	1702 GGACATCTGCATCTCCTGTGGGAGCCTCAATGTTACCCTGGAACACCCCCTCTTCGTTGG 1761
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1942 1917	Qy	2 AAGGGAGGCTGAGAAGAAAGCCAAGGTCATTGCAGGAATGAAT
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2877 ATCGTGGAGCGTGCCGGTCATCCGCCTCTTCGCTCCGCTGAAGAATATTTTGCTTG
                                                                           3174 CTATCTAAAAAGCAAAATAGGC-CCCTCCTTCTTCCCCT---CCGGTCCTAGGAGGCG
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                                                     2962 TGTGTAAGGGACATGGGGGCAAACTGAGGTAGCGA----CACAAAGTTAAACAAACAAAC
                                                                                                                         ----- AAAAAACACAAAACATAATAAAACACCAAGAACATGAGGATGGAGAGAAGTATCA
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiavascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel genes (ABL89449-ABL90853) and proteins MBB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. bereat and ovarian cancer and other cancers of the adrenal gland, bone, bone arrow, breast, gastrointestinal tract, liver, ung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                           4122
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                                    4027 CTAGATGAGGTGGTCGGGCCCGTGGACAGCTGAGAGTGGGATTCATCCAGACTCATGCAA 4086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders
                                                                       3949 TCAGCTGAGGTGGTCGGACCCTGGGGAAGCTGAGTGTGGAATTTATCCAGACTGCGTGC
                                                                                                                                   4009 AATAACCTTAGAATATGAATCTAAAATGACTGCCTCAGAAAAATGGC-----TTGAGAA
                                                                                                            4087 TAACCCTTTGATTGTTTTCTAAAAGGAGACTCCCTCGGCAAGATGGCAGAGGGTACGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polynucleotide SEQ ID NO 953.
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Matches 2781; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : The sequence data for this patent did not form part of ted specification, but was obtained in electronic format WIFO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                        CATTCAGGTGGACCGCTACATTGCCTCGGAGGTGTGTGAGGACTCCATCACGGTGGGCAT
                                                                                                                                                                                      CCGGGTGCTGTCTCTTTGATGGAATCGCTACAGGGCTCCTGGTGCTGAAGGACTTGGG
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                                                                                                                                                                                                                                                                                                            GCTGCGGCGGCGAGAGGACTGGCCCTCCCGGCTCCAGATGTTCTTCGCTAATAACCACGA
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TATCCAGGAGTGGGGCCCATTCGATCTGGTGATTGGGGGGCAGTCCCTGCAATGACCTCTC
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                                             GGTGCGGCACCAGGGAAGATCATGTACGTCGGGGACGTCCGCAGCGTCACACAGAAGCA
                                                                         GGTGCGGCACCAGGGGAAGATCATGTACGTCGGGGACGTCCGCAGCGTCACACAGAAGCA 2310
                                                                                                      CATTCAGGTGGACCGCTACATTGCCTCGGARGTGTGTGAGGACTCCATCACGGTGGGCAT
                                                                                                                                                                    CCGGGTGCTGTCTCTTTGATGGAATCGCTACAGGGCTCCTGGTGCTGAAGGACTTGGG
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Pred. No. 0;
5; Mismatches
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ממ	TATCCAGGAGTGGGGCCCATTCGATCTGGTGATTGGGGGCAGTCCCTGCAATGACCTCTC 9	806
γQ	2371 CATCGTCAACCCTGCTCGCAAGGGCCTCTACGAGGGGCACTGGCCGGCTCTTCTTGAGTT 2	2430
Db	CATCGTC	896
Qy	2431 CTACCGCCTCCTGCATGATGCGCGGCCCAAGGAGGGAGGAGATGATCGCCCCTTCTTCTGGCT 2	2490
Db	969 CTACCGCCTCCTGCATGATGCGCGGCCCAAGGAGGAGATGATCGCCCCTTCTTCTGGCT 1	1028
D Oy	2491 CTTTGAGAATGTGGCCATGGGCGTTAGTGACAAGAGGGACATCTCGCGATTTCTCGA 2	2550 L088
<u>ح</u>	551 GTCCAACCCTGTGATGATTGATGCCAAAGAAGTGTCAGCTGCACACAGGGCCCGCTACTT	9
Db	089 GTCCAACCCTGTGATGATTGATGCCAAAGAAGTGTCAGCTGCACACACA	14
δλ	CTGGGGTAACCTTCCCGGTATGAACAGGCCGTTGGCATCCACTGTGAATGAT	2670
ממ	1149 CTGGGGTAACCTTCCCGGTATGAACAGGCCGTTGGCATCCACTGTGAATGATAAGCTGGA	1208
. 8	1 GCTGCAGGAGTGTCTGGAGCATGGCAGGATAGCCAAGTTCAGCAAAGTGAGGACCATTAC	73
dd	209	1268
Db Qy	2731 TACGAGGTCAAACTCCATAAAGCAGGGCAAAGACCAGCATTTTCCTGTCTTCATGAATGA	2790 1328
Qy	2791 GAAAGAGGACATCTTATGGTGCACTGAAATGGAAAGGGTATTTGGTTTCCCAGTCCACTA 2	2850
ממ	1329 GAAAGAGGACATCTTATGGTGCACTGAAATGGAAAGGGTATTTGGTTTCCCAGTCCACTA 1	1388
, V	851 TACTGACGTCTCCAACATGAGCCGCTTGGCGAGGCAGAGACTGCTGGGCCGGTCATGGAG	91
- 5	303 TWCTRACGICICCAACAIGAGCCGCIIGGCGAGGCAGAGACIGCIGGGCCGGICAIGGAG	4.
Qy da	2911 CGTGCCAGTCATCCGCCACCTCTTCGCTCCGCTGAAGGAGTATTTTGCGTGTGTGT	2970
γQ	2971 GACATGGGGGCAAACTGAGGTAGCGACACAAAGTTAAACAAAC	3030
ממ	1509 GACATGGGGGCAAACTGAGGTAGCGACACAAAGTTAAACAAAC	1568
Db Qy	3031 CATAATAAAACACCAAGAACATGAGGATGGAGAGAGAAGTATCAGCACCCAGAAGAGAAAAA 3	3090 1628
 0 _V	091 GGAATTTAAAACAAAAACCACAGAGGCGGAAATACCGGAGGGCTTTGCCTTGCGAAAAGG	15
Db 45	629 GGAATTTAAAACAAAAACCACAGAGGGCGGAAATACCGGAGGGCTTTGCCTTGCGAAAAAGG	68
γQ	3151 GTTGGACATCATCTCCTGATTTTTCAATGTTATTCTTCAGTCCTATTTAAAAACAAAACC 3	3210
ממ	89 GTTGGAC	1748
γQ	3211 AAGCTCCCTTCCCTTCCCCCCCTTTCTTTTTTTCGGTCAGACCTTTTATTTTCTACT 3	3270
DB DB	749	808
δ δ	271 CTTTTCAGAGGGGTTTTCTGTTTGGGGTTTTGTTTCTTGCTGTGACTGAAACAAGAA 3	LJ C
	809 CITITAWAWAAATIITTEITIGITTAAAACAAWAA	ď
g qq	3331 GGTTATTGCAGCAAAAATCAGTAACAAAAAATAGTAACAATACCTTGCAGAGGAAGGTG 3 1	3390 .928
 o _v	391 GGAGGAGAGAAAAAGGGAAATTTTTAAAGAAATCTATATATTGGGTTGTTTTTTTT	4.
	29 GGAGAGAGGAAAAAAGGAAATTCTATAGAAATCTATATATTTGGGTTTGTTTTTTTT	98

Location/Qualifiers 1152676 /*tag= a /*tag= a /product= "de novo DNA cytosine methyltransferase	qπ	90 11 80	/ rtag= d / number= 3 319.420 / tag= e	/ Dumber= 4 421.546 /*tag= f / Dumber= 5	547708 /*tog= g /number= 6 769927 /*tog- h	/number 7 /number 7 9281035 /*tag i	//thuber= 6 //thag= 1 /*tag= 1 //number= 9	11811240 /*tag= k /number= 10 12411366	/rumber= 11 /number= 11 1367.1411 /tag= m /-ram	//////////////////////////////////////	/#tag= 0 /#tag= 0 /number= 14 /605.1788	/"tag= p /Tumber= 15 17891873 /"tag= q /"tag= q	Admosr= lb 194.:2019 4:08= r number= 17	/*tag= s /rumber= 18 2111:-2259 /*tag= t	/number= 19 22602345 /*tag= u /number= 20	23462415 //tag= v /numbe= 21	24162534 /rtcap /number= 22	
Key	exon	exon	exon	exon	exon	exon	exon	exon exon	exon	exou	ex on	exon	exon	exon exon	exon	exon	exon	exon
	FT FT FT	TA . TA TA													TA 44	TA TA	15 TE	TH.
Oy 3451 TCPTTTTTGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	3510		OY 3630 GAACCCAGTTAGCAGCAGGAGACGAGAACACCACACAAGACATTTTCTACAGTATTTC 3689 D 2166 GAACCCAGTTAGCAGCAGAGAGAGAACACCACACAAGACATTTTCTACAGTATTTC 2225	OY 3690 AGGIGCCTACCACACAGAAACCTTGAAGAAAATCAGTTTCTAGAAGCCGCTGTTACCTC 3749 Db 2226 AGGIGCCTACCACACAGGAAACCTTGAAGAAAATCAGTTTCTAGAAGCCGCTGTTACCTC 2285	OY 3750 TIGITIACAGTITATATATATATGATAGATAGAGATATATATATATAAAAGGTACTGTTAA 3809 DD 2286 TIGITIACAGTITATATATATATGAGATATGAGATATATATATATATA	OY 3810 CTACTGTACAACCCGACTTCATAATGGTGCTTTCAAACAGCGAGATGAGTAAAAACATCA 3869	OY 3870 GCTTCCACGTTGCCTTCTGCGCAAAGGGTTTCACCAAGGATGGAGAAAGGGAGACACTT 3929 Db 2406 GCTTCCACGTTGCCTTCTGCGCAAAGGGTTTCACCAAGGATGGAGAAAGGGAAGAGAGTT 2465	OY 3930 GCAGATGGCGCGTTCTCACGGTGGGCTCTTCCCCTTGGTTTGTAACGAAGTGAAGGAGGA 3989 Db 2466 GCAGATGGCGCGTTCTCACGGTGGGCTCTTCCCCTTGGTTTGTAACGAAGTGAAGGAGGA 2525	QY 3990 GAACTIGGGAGCCAGGITCTCCCTGCCAAAAAGGGGGCTAGATGAGGTGGTCGGGCCCGT 4049 DD 2526 GAACTIGGGAGCCAGGITCTCCCTGCCAAAAAGGGGGCTAGATGAGGTGGTCGGGCCCGT 2585	OY 4050 GGACAGCTGAGAGTGGGATTCATCCAGACTCATGCAATAACCCTTTGATTGTTTTCTAAA 4109	QY 4110 AGGAGACTCCCTCGGCAAGATGGCAGAGGTACGGAGTCTTCAGGCCCAGTTTCTCACTT 4169 Db 2646 AGGAGACTCCCTCGGCAAGATGGCAGAGGTACGGAGTCTTCAGGCCCAGTTTCTCACTT 2705	Oy 4170 TAGCCAATTCGAGGGCTCCTTGTGGTGGGATCAGAACTAATCCAGAGTGTGGGGAAAGTGA 4229 Db 2706 TAGCCAATTCGAGGGCTCCTTGTGGTGGGATCAGAACTAATCCAGAGTGTGGGAAAGTGA 2765	Oy 4230 CAGTCAAAACCCCACTGGAGCAAATAAAAAAACATACAAAACGTA 4275 	RESULT 4 AAZ37098 ID AAZ37098 standard; DNA; 4145 BP.	entrv)	Бu	KW De novo DNA cytosine methyltransferase; DNMT3B1; neoplastic disorder; KW carcinoma; Barcoma; leukaemia; DNA methylation; ss. vv	OS Homo sapiens. XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a human de novo DNA cytosine cc methyltransferase designated DNMT3B1. The DNMT3B gene also produces, through alternate splicing, at least two shorter isoforms termed CC DNMT3B2 (comprising amino acids 1-355 and 376-943 and 807-853 cf AAY54058) and DNMT3B3 (comprising amino acids 1-355, 376-743 and 807-853 cf AAY54059) and DNMT3B3 (comprising amino acids 1-355, 376-743 and 807-853 cf AAY54059) and DNMT3B3 (comprising amino acids 1-355, 376-743 and 807-853 cf AAY54059) and DNMT3B3 (comprising amino acids 1-355, 376-743 and 807-853 cf AAY54059) and DNMT3B3 (comprising amino acids 1-355, 376-743 and 807-853 cf AAY54059) and DNMT3B3 (comprising amino acids 1-355, 376-743 and 807-853 cf AAY54059) and DNMT3B3 (comprising amino acids 1-355, 376-743 and 807-853 cf AAY54059) and DNMT3B3 (comprising acids 1-355, 376-743 and 807-853 cf AAY54059) and DNMT3B3 (comprising amino acids 1-355, 376-743 and 807-853 cf AAY54058) and DNMT3B3 (comprising polymorphides can be accomplianted to disprose, or determine susceptibility to neoplastic disorders, by assaying for complementation susceptibility to neoplastic disorders, by assaying for complementation acids of the polymorphide. The polymorphide can also be used for in vitro de novo methylateion of DNA. CC such in vitro methylated in vitro de novo methylated in vitro may be introduced into a cell/organism to increase or decrease expression of a desired polypeptide for which the native DNA is compression of a desired polypeptide for which the native DNA is compression and beneathylated are useful to detect and purify the polypeptide cor therapeutically e.g. to treat neoplastic disorders. The complementation are useful to produce probes and primers which are useful cor diagnostically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Sim
Matches 1244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mouse and human polypeptides, useful to treat and diagnose neoplastic disorders e.g. carcinomas, sarcomas and leukemias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 1D; 114pp; English.
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24-JUL-1998;
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                                                                                   CTGGCATGCGGTGGGTCCAGTGGTTTTGGCGATGGCAAGTTCTCCG
                                                                                                                        AGTACGAGGACGGCCGGGGCTTTGGCATTGGGGAGCTGGTGTGGGGGAAACTGCGGGGCT 1136
                                                                                                                                                                                                                                                                                                                                           AGCAGGGGGCATGGAGTCCCCCGCAGGTGGAGGCAGACAGTGGAGATGGAGACAGTTCAG 760
                                                                                                                                                                                                                                                                                                                                                                                     AGCCCGTGGGGTCCGATGCTGGGGACAAGAATGCCACCAAAGCAGGCGATGACGAGCCAG 1076
AACTGGTGGCACTGGGGGTTCAGCCAGCACTTTAATTTGGCCACCTTCAATAAGCTCG
                                       AGCTGATGCCGCTGAGCTCGTTTTGCAGTGCGTTCCACCAGGCCACGTACAACAAGCAGC 1316
                                                                                                                                                                      TCTCCTGGTGGCCCGCCATGGTGGTGTCTTGGAAGGCCACCTCCAAGCGACAGGCTATGT
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Pred. No. 1e-145;
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ATCGTCAACCCTGCTCGCAAGGGCCTCTACGAGGGCACTGGCCGGCTCTTCTTTGAGTTC
                                          ATTGAAGAATGGGGCCCATTTGACTTGGTGATTGGCGGAAGCCCATGCAACGATCTCTCA
                                                                                                                                       GTGAAGCACGAGGGGAATATCAAATACGTGAACGACGTGAGGAACATCACAAAGAAAAAT
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                                                                                       ATCCAGGAGTGGGGCCCATTCGATCTGGTGATTGGGGGGCAGTCCCTGCAATGACCTCTCC
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                                                                2140 TACCACCTGCTGAATTACTCACGCCCCAAGGAGGGTGATGACCGGCCGTTCTTCTGGATG
                                                                                                                                2200 TTTGAGAATGTTGTAGCCATGAAGGTTGGCGACAGAGAGGGACATCTCACGGTTCCTGGAG
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/product= "de novo DNA cytosine methyltransferase
Dnmt3b1"
                                               2432 TACCGCCTCCTGCATGATGCGCGCCCCAAGGAGGAGGATGATCGCCCCTTCTTCTGGCTC
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269..2848
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24-JUL-1998;
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The present sequence encodes a murine de novo DNA cytosine methyltransferase designated Dnmt3b1. The Dnmt3b gene also produces, through alternate splicing, at least two shorter isoforms of 840 and 777 amino acid residues, termed Dnmt3b2 and Dnmt3b3 (sequences of therapeutically), especification). The polypeptides can be administered cot given in the specification). The polypeptides can be administered correct diseases associated with DNA cytosine methyltransferase, such as neoplastic disorders e.g. carcinomas, sarcomas and leukemias. They can be used to disagnose, or determine susceptibility to neoplastic disorders, by assaying for polypeptide expression levels in mammalian cells/body fluids. They are useful to screen for compounds inhibiting/activating the colpypeptide can also be used for in vitro de novo methylation of DNA. Such in vitro methylation may be used to direct or regulate DNA expression in biological systems, e.g. recombinant DNA methylated in vitro methylation of a desired polypeptide for which the native DNA is under-methylated or not methylated. The polypeptide so not methylated or the polypeptides can also be used to produce antibodies which are useful to detect and purify the polypeptide or therapeutically e.g. to treat neoplastic disorders. The colpyper or the displace produce probes and primers which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1255
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                                                                                                     New mouse and human polypeptides, useful to treat and diagnose neoplastic disorders e.g. carcinomas, sarcomas and leukemias
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                                                                                                                                                                                           Claim 9; Fig 1B; 114pp; English.
                        WPI; 2000-106298/09.
P-PSDB; AAY54056.
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ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB7893 to ABB79004 represent proteins encoded by the ABQ60776 to ABG60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polynucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I) and for determining the phenotype of cells in a sample

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of cells from a parient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists.
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                                                                                                                                                                              Query Match

14.3%; Score 613; DB 24; Length 709;
Best Local Similarity 94.5%; Pred. No. 3.6e-115;
Matches 664; Conservative 0; Mismatches 33; Indels 6
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                                                                                                                                                 Sequence 709 BP; 163 A; 177 C; 193 G; 168 T; 8 other;
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AAH32943 to AAH37155 and AAG73514 to AAG77788 represent human colon cancer—associated nucleic acid molecules (N) and proteins (P), where cancer antigens are collectively known as colon cancer antigens. The colon cancer antigens have eyclostatic acidity and can be used in gene cancer antigens have eyclostatic acidity and can be used in gene cancer antigens have eyclostatic acidity and be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders or associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing to rocal in a patient's genome that affect the activity of P by expressing to express the proteins or to supplement the patients own production of P. C. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB37789 represent sequences used in the exemplification of the present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
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Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; ss.
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                                                                                                                                                                                                                                                     reproductive
                                                                                                                                                                                                                                                                                                                                                standard; cDNA; 622
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   2000US-0179065.
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2000US-0184664.
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2000US-022527
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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a coding sequence of the invention.
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                                                                                                                      Ouery Match
Best Local Similarity 98.0%; Pred. No. 4.1e-93;
Matches 540; Conservative 2; Mismatches 6; Indels 3; Gaps
                                                                                                                                                                                                                                 2 CCAGCCTTCTGGCCCTAAGGGCCTAGAGCCACCAGAAGAAGAAGAAGAATCCCTACAAAGA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                   182 CACAAGAGAGCGGCTGGTGTACGAGGTGCGGCAGAAGTGCCGGAACATTGAGGACATTTG
                                                                                       Sequence 622 BP; 154 A; 161 C; 189 G; 112 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA sequence SEQ ID NO:11099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 272; 1297pp + Sequence Listing; English.
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13 - OCT - 2000 | 2000US - 0239935 | 20 - OCT - 2000 | 2000US - 0241096 | 20 - OCT - 2000 | 2000US - 0241096 | 20 - OCT - 2000 | 2000US - 0241096 | 20 - OCT - 2000 | 2000US - 0241096 | 20 - OCT - 2000 | 2000US - 0241196 | 20 - OCT - 2000 | 2000US - 0241196 | 20 - OCT - 2000 | 2000US - 0241196 | 20 - OCT - 2000 | 2000US - 0241196 | 20 - OCT - 2000 | 2000US - 0241809 | 20 - OCT - 2000 | 2000US - 0241809 | 20 - OCT - 2000 | 2000US - 0241809 | 20 - OCT - 2000 | 2000US - 0241806 | 20 - OCT - 2000 | 2000US - 024647 | 20 - OCT - 2000 | 2000US - 024647 | 20 - OCT - 2000 | 2000US - 024647 | 20 - OCT - 2000 | 2000US - 024647 | 20 - OCT - 2000 | 2000US - 024647 | 20 - OCT - 2000 | 2000US - 024647 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 024652 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT - 2000 | 2000US - 02492 | 20 - OCT | 2000US
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05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0251988.
06-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
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05-JAN-2001; 2001US-0259678.
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P-PSDB; AAM94301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers sets can be used in antisense therapy and in gene therapy. The primers sets can be used in antisense polynucleotides, particularly full length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH3166 to AAH13628 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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11-JAN-2000; 2000JP-0118776
02-MAY-2000; 2000JP-0183767
09-JUN-2000; 2000JP-0241899
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                                                                     GCCTTCTGGCCCTAA---
                                                                                                                                                                                AAGCCCATGTTGGAGTGGGCCCACGGGGCTTCAAGCCCACTGGGATCGAGGGCCTCAAA
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Sugiyama
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                                    -CAAGGAAATACGAGAACAAGACTCGAAGACGCACAGCTGACGACTCAGCCAC
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1 T, Wakama
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Wakamatsu
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1 A, Naga
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Nagai K,
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Otsuki
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Composition having probes which comprise part of gene sequence encoding proteins associated with cell proliferation useful as hybridizable array elements in Microarrays to monitor expression of target polynucleotide
                                                                                                            225 CGGCACCAGGGGAAGATCATGTACGTCGGGGACGTCCGCAGCGTCACACAGAAGCATATC 2314
                                                                                                                                                                                                                            2315 CAGGAGTGGGGCCCATTCGATCTGGTGATTGGGGGCAGTCCCTGCAATGACCTCTCCATC 2374
                                  61 AAGGTAGGAAAGTACGTCGCTTCTGAAGTGTGTGAGGAGTCCATTGCTGTTGGAACCGTG 120
                                                                                                                                              121 AAGCACGAGGAAATATCAAATACGTGAACGACGAGGAACATCACAAGAAAAATATT 180
                                                                                                                                                                                                                                                                                 181 GAAGAATGGGGCCCATTTGACTTGGTGATTGGCGGAAGCCCATGCAACGATCTCTCAAAT 240
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2195 CAGGTGGACCGCTACATTGCCTCGGAGGTGTGTGAGGACTCCATCACGGTGGGCATGGTG
                                                                                                                                                                                                                                                                                                                                            23.75 GTCAACCCTGCTCGCAAGGGCCTCTACGAGGGCACTGGCCGGCTCTTCTTTGAGTTCTAC
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Baughn MR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerates chain refection (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The configuration of the polymerectides are also used in diagnostics as expressed sequence tags of the formity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving an applyagation in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical insolution and polymucleotide sequences have applications in capposition and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations of mutations and produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human DNA and diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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8.0%; Score 344.2; DB 23; Length
Best Local Similarity 75.0%; Pred. No. 2e-60;
Matches 430; Conservative 0; Mismatches 143; Indels
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                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #21969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification, but was obtained in electroni
at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                              AASB6165 standard; cDNA; 711 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT;
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23-AUG-2000; 2000US-0649167.
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1440 TGTGCACTACA 1450
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P-PSDB; ABG21978.
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(HYSE-) HYSEQ INC.

biodiversity

2135

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WO200175067-A2. Homo sapiens.

11-OCT-2001

13-FEB-2002

AAS86165;

AAS86165

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RESULT 12
AAT21884
ID AAT21
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AC AAT21
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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   14-AUG-1996
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nes 416; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAAAGTACAGACAATAACCACCAAGTCGAACTCGATCAAACAGGGGGAAAAACCAACTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCACAGGGCCCGATACTTCTGGGGCAACCTACCCGGGATGAACAGGCCCCGTGATAGCAT
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                                                                                                                            standard; cDNA to mRNA; 301
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(first entry)
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Pred. No. 3e-5
0; Mismatches
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Gene signature;
human; cloning;
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                                                                                                                                                                                Human
                                                                                                                                                                                gene signature HUMGS03426
                                                                                                                                                                re; messenger RNA; mRNA; relative abundance; frequency; ng; mapping; non-biased library; diagnosis; detection; abnormal cell function; ss.
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Matsubara K, 12-NOV-1993; 11-NOV-1994; 01-JUN-1995. (MATS/) MATSUBARA K. (OKUB/) OKUBO K. Okubo 93JP-0355504 94WO-JP01916

Identifying gene signatures in 3'-directed human cDNA library - e. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human Ġ

WPI; 1995-206931/27.

Claim 1; Page 991-992; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. CC double-stranded DNA) which comprises one of the 7837 "GS" sequences CC given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) CC sequences were obtained from 3'-directed cDNA libraries prepared CC from various human tissues; synthesis of cDNA was initiated from the CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-CC untranslated sequence is unique to a particular mRNA species, almost CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of CC different mRNAs in the particular tissue from which it was derived. CC determined (sep. using primers and probes derived from the GS cequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 301 BP; 96 A; 65 C; 63 G; 66 T; 11 other;

Query Match Best Local (

Similarity

6.6**%**; 95.3**%**;

Length

301;

밁 S 밁 S ₽ á 밁 Ş Š Matches 3759 3639 3699 3579 181 121 61 **_** CTCCCAGCCACTGAGCTGTCGTGCCAGCACCATTCCTGGTCACGCAAAACAGAAACCCCAGT 3638 GTTTATATATATATGATAGATATGNGNTATATATATAAAAAGGTACTGTTAACTACTGTAA GTTTATATATATATGATAGATATGAGATATATATATAAAAGGTACTGTTAACTACTGTAC 3818 CCACACAGGAAACCTTGAAGAAAATCAGTTTCTAGAAGCCGCTGTTACCTCTTGTTTACA 3758 TAGCAGCAGGAGACGAGACACCACACAGACATTTTTCTACAGTATTTCAGGTGCCTA 180 TAGCAGCAGGAGAGACACACACACACACACATTTTTCTACAGTATTTCAGGTGCCTA 3698 CTNCCAGCCACTGAGCTGNCGTGCCAGCACCATTCCTGGTCACGCAAAACAGAACCCATT GATCAGATAGGAGCACAAGCAGGGGACGGAAAGAGAGACACTCANGCGGCAGCATTCC 287; Conservative 0 Score 285.2; DB 16; Pred. No. 1.5e-48; 0; Mismatches 14; Indels 0 Gaps 120 3578 240 60 0

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153 CGCCAAGATGCCAGAGGGTACTTCAGGCCCAGTTTCTCACTTTAGCCAATTCGA 94
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20-SEP-2000, 2000US-2331331F.
20-SEP-2000, 2000US-2341346.
20-SEP-2000, 2000US-234052P.
22-SEP-2000, 2000US-234550P.
22-SEP-2000, 2000US-234550P.
25-SEP-2000, 2000US-234550P.
25-SEP-2000, 2000US-234560P.
25-SEP-2000, 2000US-235034P.
25-SEP-2000, 2000US-23503P.
25-SEP-2000, 2000US-23503P.
25-SEP-2000, 2000US-23503P.
26-SEP-2000, 2000US-23503P.
27-SEP-2000, 2000US-23503P.
27-SEP-2000, 2000US-23503P.
27-SEP-2000, 2000US-23503P.
28-SEP-2000, 2000US
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2000US-237598P.
2000US-237604P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                 Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4002 CAGGITCICCCIGCCAAAAAGGGGGGCTAGAIGAGGIGGICGGGCCCGIGGACAGCIGAGA 4061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4062 GTGGGATTCATCCAGACTCATGCAATAACCCTTTGATTGTTTTCTAAAAGGAGACTCCCT 4121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4122 CGGCAAGATGGCAGAGGGTACGGAGTCTTCAGGCCCAGTTTCTCACTTTAGCCAATTCGA 4181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 CAGGTTCTCCCTGCCAAAAGGGGGCTAGATGAGGTGGTCGGGCCCGTGGACAGCTGAGA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 GTGGGATTCATCCAGACTCATGCAATAACCCTTTGATTGTTTTTCTAAAAGGAGACTCCCT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alvares C, Peres-Da-Silva S, Vockley JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 273 BP; 59 A; 74 C; 62 G; 78 T; 0 other;
                                                                                                                                                                                                                                                                               Gene #3887 used to diagnose liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1, SEQ ID NO 3887; 298pp; English.
                                                                                                                                   ABN97389/с
ID ABN97389 standard; DNA; 273 ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-2001; 2001WO-US30589.
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                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-426119/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200229103-A2
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                             301 A 301
                                                                                                                                                                                              ABN97389;
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                                                                                                        RESULT 13
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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.
4182 GGGCTCCTTGTGGTGGGATCAGAACTAATCCAGAGTGTGGGAAAGTGACAGTCAAAACCC 4241
                                                                   93 GGGCTCCTTGTGGGTGGGGATCAGAACTAATCCAGAGTGTGGGGAAAGTGACAGTCAAAAACCC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stomach cancer related gene sequence SEQ ID NO:2565.
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RESULT 15
ABA20255
ID ABA20
XX
AC ABA20
DT 23-JA
XX
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                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical cagent to be tested for anti-neoplastic activity, determining a change in capression of at least one gene (I) of a signature gene set, where (I) cc comprises a sequence (S) selected from 8447 sequences (given in ABL61664 cc to ABL70110), or is at least 95% identical to (S), where a change in capression is indicative of anti-neoplastic activity. (I) has cytostatic cativity and can be used in gene therapy. M1 can be used for screening cc an anti-neoplastic agent, and can be used for producing a product which cs the data collected with respect to the anti-neoplastic agent as a cresult of M1, and the data is sufficient to convey the chemical cs tructure and/or properties of the agent. M1 can be used in the ct reatment of cancer such as colon, breast, stomach, lung, thyroid, cesophageal, ovarian, kidney, prostate or pancreatic cancer, cc adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, cc infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
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Best Local S
Matches 273
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03-OCT-2000;
01-NOV-2000;
01-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4002 CAGGTTCTCCCTGCCAAAAAGGGGGGCTAGATGAGGTGGTCGGGCCCGTGGACAGCTGAGA 4061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening for anti-neoplastic agent involves exposing cells to chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature ger
               Human nervous system related polynucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 273 BP; 59 A; 74 C; 62 G; 78 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-188264/24.
                                                                                                                            ABA20255 standard; DNA; 546 BP
                                                     23-JAN-2002
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                                                                                                                                                                                                                                                                                            93
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                                                                                                                                                                                                                     CACCTGGAGCAAATAAAAAAACATACAAAACGT
                                                                                                                                                                                                                                                      CACCTGGAGCAAATAAAAAAAACATACAAAACGT 4274
                                                                                                                                                                                                                                                                                          GGGCTCCTTGTGGTGGGATCAGAACTAATCCAGAGTGTGGGAAAGTGACAGTCAAAACCC
                                                                                                                                                                                                                                                                                                                             GGGCTCCTTGTGGTGGGATCAGAACTAATCCAGAGTGTGGGAAAGTGACAGTCAAAACCC 4241
                                                                                                                                                                                                                                                                                                                                                                 CGGCAAGATGGCAGAGGGTACGGAGTCTTCAGGCCCAGTTTCTCACTTTAGCCAATTCGA
                                                                                                                                                                                                                                                                                                                                                                                      CGGCAAGATGGCAGAGGGTACGGAGTCTTCAGGCCCAGTTTCTCACTTTAGCCAATTCGA 4181
                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGGATTCATCCAGACTCATGCAATAACCCTTTGATTGTTTTCTAAAAGGAGACTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGGATTCATCCAGACTCATGCAATAACCCTTTGATTGTTTTCTAAAAGGAGACTCCCT 4121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGTTCTCCCTGCCAAAAAAGGGGGCTAGATGAGGTGGTCGGGCCCGTGGACAGCTGAGA 214
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Weaver 2
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; 2000US-237608P.
; 2000US-244867P.
; 2000US-245084P.
                                                 (first entry)
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Pred. No.
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antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; ds

Homo sapiens.

WO200159063-A2

16-AUG-2001

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2000US-0225757, 2000US-0225757, 2000US-0225758, 2000US-0225759, 2000US-0226279. 2000US-0226681 2000US-0226868 5-0226279 5-0226681

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The invention relates to novel genes (ABA11004-ABA21514) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and (ant)agonists are useful. The mucleic acids, proteins, antibodies and (ant)agonists are useful. The mucleic acids, proteins, antibodies and (ant)agonists are useful. The mucleic acids proteins, and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy, and (f) infections diseases such as viral, bacterial, fungal and parasitic infections.

Conversion of the patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                               Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          586 GGGTGCAGCTGAGACCCTGCCTGAAGCCTCAAGAGCAGTGGAAAATGGCTGCTGCACCCC 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   466 CCAGGACTCAGGCGCCTCAGAGCTATTACCCAATGGGGACTTGGAGAGAGCGGAGTGAGCC 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGCCAGAGGAGGGGAGCCCTGCTGGGGGGCAGAAGGGCGGGGGCCCCCAGCAGAGGGAGA 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 546 BP; 133 A; 137 C; 171 G; 105 T; 0 other;
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08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0259090.
                                                                                                                                                                                                Ruben
                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                Barash SC,
                                                                                                                                                                                                                                       WPI; 2001-541565/60.
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